

GenCore version 4.5  
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## OM protein - protein search, using sw model

Run on: September 13, 2002, 10:15:56 ; Search time 14.7 Seconds

Perfect score: 1404.056 Million cell updates/sec

Title: US-09-695-293-42  
Sequence: 1 METKGVHSLPSEGIDMERRWG... ... FLYFAPDVLVNELLARYREG 845  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters:

231628

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

Issued\_Patents\_AA: \*  
1: /cgn2\_6/prodata/2/1aa/5A\_COMB\_pep: \*  
2: /cgn2\_6/prodata/2/1aa/5B\_COMB\_pep: \*  
3: /cgn2\_6/prodata/2/1aa/6A\_COMB\_pep: \*  
4: /cgn2\_6/prodata/2/1aa/6B\_COMB\_pep: \*  
5: /cgn2\_6/prodata/2/1aa/PCTUS\_COMB\_pep: \*  
6: /cgn2\_6/prodata/2/1aa/backfiles1.pep: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4385	99.2	984	4	US-08-764-870-15
2	4385	99.2	984	4	US-08-980-115-15
3	856	19.4	777	4	US-08-764-870-13
4	856	19.4	777	4	US-08-980-115-13
5	845.5	19.1	795	1	US-07-716-837C-5
6	801	18.1	933	4	US-08-764-870-14
7	801	18.1	933	4	US-08-980-115-14
8	732.5	16.6	363	6	US-23606-6
9	726	16.4	918	4	US-09-041-886-11
10	713.5	16.1	356	6	US-08-764-870-16
11	686.5	15.5	452	4	US-08-980-115-16
12	686.5	15.5	452	4	US-08-764-870-12
13	445.5	10.1	595	4	US-08-980-115-12
14	445.5	10.1	595	4	US-08-980-115-12
15	442.5	10.0	591	2	US-08-836-620A-17
16	442.5	10.0	595	4	US-09-041-886-35
17	438	9.9	596	2	US-08-836-620A-16
18	417	9.4	548	4	US-09-139-617-1
19	410	9.3	418	3	US-09-041-000-6
20	410	9.3	435	3	US-09-040-008-2
21	410	9.3	435	4	US-09-500-654-2
22	410	9.3	458	3	US-09-141-000-4
23	406.5	9.2	484	2	US-08-836-620A-14
24	406.5	9.2	485	2	US-08-836-620A-15
25	405	9.2	384	2	US-08-836-620A-15
26	404.5	9.1	485	2	US-08-836-620A-3
27	403.5	9.1	484	2	US-08-836-620A-13

## ALIGNMENTS

RESULT 1  
US-08-764-870-15  
; Sequence 15, Application US/08764870  
; Patent No. 6236946  
GENERAL INFORMATION:  
; APPLICANT: Scanlan, Thomas S  
; APPLICANT: Baxter, John D  
; APPLICANT: Fleitterick, Robert J  
; APPLICANT: Wagner, Richard L  
; APPLICANT: Kusiner, Peter J  
; APPLICANT: Aprilletti, James W  
; APPLICANT: West, Brian  
TITLE OF INVENTION: Nuclear Receptor Ligands and Ligand  
TITLE OF INVENTION: Binding Domains  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Cooley Godward  
STREET: Five Palo Alto Square,  
CITY: Palo Alto  
STATE: CA  
ZIP: 94306  
COUNTRY: USA  
ZIP: 94306  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC Compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/764, 870  
FILING DATE: 13-DEC-1996  
CLASSIFICATION: 530  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 60/008, 540  
FILING DATE: 13-DEC-1995  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 60/008, 543  
FILING DATE: 13-DEC-1995  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 60/008, 606  
FILING DATE: 14-DEC-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Nakamura, Jackie N  
REGISTRATION NUMBER: 35,966  
REFERENCE/DOCKET NUMBER: UCAL-246-010US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 943-5000  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 984 amino acids  
TYPE: amino acid

STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-764-870-15

APPLICANT: Baxter, John D.  
APPLICANT: Fletterick, Robert J.  
APPLICANT: Wagner, Richard L.  
APPLICANT: Kushner, Peter J.  
APPLICANT: Kroll, James W.

	Query Match	99.2%	Score	4385	DB	4	Length	984
Best Local Similarity	100.0%	Pred.	No.	0	Mismatches	0	Indels	0
Matches	837	Conservative	0	0				0
a	1 MERKGYSILPEGLDMERWKGQSQAVERSLGGPTERTDENNMEIVNVSCVSGAIPNST	60						
b	1 METGKYHSLPEGLMERWKGQSQAVERSLGGPTERTDENNMEIVNVSCVSGAIPNST	60						
b	1 OGSSEKEKELPLQLQDQNRPGILTSIDKTELESKELSATVESMGLYMDSYRDADSYE	120						
b	1 OGSSEKEKELPLQLQDQNRPGILTSIDKTELESKELSATVESMGLYMDSYRDADSYE	120						
c	121 QONQOGSMSPAKITYQNVOLKYKGNGHRPSTLSCVNTPLSFMSFGSSNGVRAI	180						
b	121 QONQOGSMSPAKITYQNVOLKYKGNGHRPSTLSCVNTPLSFMSFGSSNGVRAI	180						
c	181 VKSPIMCHEKPSVCSPLNMSTSSVCSPAGINSVSSTSASFGSPVHSITQTSPPLTCSPN	240						
b	181 VKSPIMCHEKPSVCSPLNMSTSSVCSPAGINSVSSTSASFGSPVHSITQTSPPLTCSPN	240						
c	241 AENRGRSRSHSPAHASNVASPLSSLQSMKSSISPPPSHCSVKSPVSSNNVNTRSSSSP	300						
b	241 AENRGRSRSHSPAHASNVASPLSSLQSMKSSISPPPSHCSVKSPVSSNNVNTRSSSSP	300						

APPLICANT: Shiao, Andrew K.  
TITLE OF INVENTION: NUCLEAR RECEPTOR LIGANDS AND LIGAND BINDING DOMAINS  
FILE REFERENCE: UCAL-246/02US  
CURRENT APPLICATION NUMBER: US/08/9980,115  
CURRENT FILING DATE: 1997-11-26  
EARLIER APPLICATION NUMBER: 08/764,870  
EARLIER FILING DATE: 1996-12-13  
EARLIER APPLICATION NUMBER: 60/0008,606  
EARLIER FILING DATE: 1995-12-14  
EARLIER APPLICATION NUMBER: 60/0008,543  
EARLIER FILING DATE: 1995-12-13  
EARLIER APPLICATION NUMBER: 60/0008,540  
EARLIER FILING DATE: 1995-12-13  
NUMBER OF SEQ ID NOS: 17  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 15  
LENGTH: 984  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: DOMAIN  
LOCATION: (695)..(699)  
OTHER INFORMATION: minimal ligand binding domain

Db 301 ANINNSRCSSPSNTNRSSTLSSPASTVGCSICSPVNNAFSYTAGTSSAGSSTLRDVPP 360  
 Qy 361 SPDTQEKQAEVPPKTFEEVESEAISNGVIGQLNIVQYTRKEPDGAFSSCLGANSKNSD 420  
 Db 361 SPTQEKQAEVPPKTFEEVESEAISNGVIGQLNIVQYTRKEPDGAFSSCLGANSKNSD 420  
 Qy 421 SSFSVPVIQEESTKHSCSGTSFKGNPTVNPFPMDGSYFSFMDDKDYSSLSGLGPVPVGF 480  
 Db 421 SSFSVPVIQEESTKHSCSGTSFKGNPTVNPFPMDGSYFSFMDDKDYSSLSGLGPVPVGF 480  
 Qy 481 DGNCEGSGCPVGTQEPDDGSYPEASIFSSATVGVNNSCGQSHYRIGQGITSLSRSAR 540  
 Db 481 DGNCEGSGCPVGTQEPDDGSYPEASIFSSATVGVNNSCGQSHYRIGQGITSLSRSAR 540  
 Qy 541 DOSFOHLSFPPNTLVESWKSKGDLSSRSRDGSPVLEYIPENVSSTSRTSVSTGSSRS 600  
 Db 541 DOSFOHLSFPPNTLVESWKSKGDLSSRSRDGSPVLEYIPENVSSTSRTSVSTGSSRS 600  
 Qy 601 KICLVCGDBASCGCHGVUTCGSKCKVFRRKAVEGOHNLYLAGRNDCIDMKRKNCPACL 660  
 Db 601 KICLVCGDBASCGCHGVUTCGSKCKVFRRKAVEGOHNLYLAGRNDCIDMKRKNCPACL 660  
 Qy 661 OKCLOQAGMNLGARKSKKKLGKLGTHEQQQQQPPPPPPPPQOSEEGTTYIAPAKEPSN 720  
 Db 661 OKCLOQAGMNLGARKSKKKLGKLGTHEQQQQQPPPPPPPPQOSEEGTTYIAPAKEPSN 720  
 Qy 721 TALVQPLSITSRALTSPMVNLENIEPELVYAGYDSSKDTAEMLSTLNACKOMIQV 780  
 Db 721 TALVQPLSITSRALTSPMVNLENIEPELVYAGYDSSKDTAEMLSTLNACKOMIQV 780  
 Qy 781 VPKWAKVVLPGFKNLPLEDTTLIQUSWMCISSPSLWSRWSKHTNSOFLYAPDLVNE 837  
 Db 781 VPKWAKVVLPGFKNLPLEDTTLIQUSWMCISSPSLWSRWSKHTNSOFLYAPDLVNE 837





PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 60/008, 606  
 FILING DATE: 14-DEC-1995  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Nakamura, Jackie N  
 REFERENCE NUMBER: UCAL-246/01US  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (650)843-5000  
 INFORMATION FOR SEQ ID NO: 14:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 933 amino acids  
 STRANDEDNESS:  
 TOPOLogy: linear  
 MOLECULE TYPE: protein  
; US-08-764-870-14

Query Match 18:1%; Score 801; DB 4; Length 933;  
 Best Local Similarity 29.5%; Pred. No. 4.8e+51;  
 Matches 253; Conservative 95; Mismatches 221; Indexes 288; Gaps 37;

QY 191 SPSVCSPLIMTSSCSPAG---INSVSSSTASFGSPFHSPHTQG---PLTC---SPNA 241  
 Db 20 SPEVGSPL---LCRPAAGPFPGSOTSDTLPESATIS---LDGLFLPRPCQGDPSD 71

QY 242 EN-----ROSRSHSPAHASNNGVPLSSP-----LSSMKSSISSPPSHCSVKSPV 285  
 Db 72 EKTQDQSISSDVCGAYSRERATRGAGGSSSSPFEDKSILDSVLDTLAR----- 121

QY 286 SSPNNVTLKSSVSAPPNINNSRVSV-----PNTNNRNLSSPAASTVGSCSP 336  
 Db 122 SGPG---QSOPSPF---CEVTSKCLFGPELPED-----PFAAPATORVLSP 163

QY 337 VNFAFSYITASGTSTAGSSTIRDVPP---SPDTo-----EKGAAQEVPEP-----KTE 378  
 Db 164 LMSR-SGCKVGDSSGTAHHKVPLRGLSPAROLLIPASESPHNSGAPVPKPSOAAVE 222

QY 379 EVEAISANSQVTQQLNIVQYIKP-----DGAFSSSC----LGGNISKI NSDSSFSV 425  
 Db 223 EEDSSESESERASGL-----LKGPRALGAAAGSGAACPPGAAGGYVALPKEDRSRA 277

QY 426 P---IKOPS-----TKHSCSGTSFKG----- 443  
 Db 278 PRVALVEQDAPMAGRSPATTVMDFIHVPIPLNHALLAARTROLLEDSEYDGAGAGS 337

QY 444 -----NETVNPP-----FMQCSYFSMDKD----- 465  
 Db 338 AFAPPRTSPCASCSTPVAVGDFPDCAYPPDAEPKDDAYPLYSDFOPPALIKEBEEGAES 397

QY 466 -----YSS-SGI-----LGPPV----- 481  
 Db 398 ARSPRSVYVAGANAAFPDPFLGPPLPRATPSRPGCAAVAAPASASVASSSST 457

QY 482 GNC-----EGSGGPVTKOEPDGSYYPEASISATTAVGNGGOSPHY-RIGA 529  
 Db 458 LECLYKARGAPPOQFPAPPCKAPGAGSCLIPRDGLPESITASAANAGAPALYPALGL 517

QY 530 QGTISLSRSARDOSFOHISSFPPNTLVESWKSHGDLSSRSDCPYVLEYI-ENVSST 588  
 Db 518 NGLPOLGYQAALK---EGLPROVTP-----PYLYNLRPDEASQS 554

QY 589 LRSVSTGSSRSPSKTCVLCVGCGDEASCHYGVTCGSKVFKRAVEGOHNILCAGRNDCID 648

Db 555 PQ--YSFESLSPKICLICDEASCHYGVLTGCGSKVFKRAVEGOHNILCAGRNDCID 612

QY 649 KIRRNCPACRLRKCCQAGMVLGGRRFKFNKFVNRAVDAVLQPLGPVPNESQALSQR 672

QY 703 TYIAPAKPSVNTALVPOLISTSRALTPSPVMLENIEPETIYAGYISSKPTAENILS 767

RESULT 6

US-08-764-870-14

; Sequence 14 Application US/08764870

; Patent No. 6236846

; GENERAL INFORMATION:

; APPLICANT: Scanlan, Thomas S

; APPLICANT: Baxter, John D

; APPLICANT: Fletterick, Robert J

; APPLICANT: Wagner, Richard L

; APPLICANT: Kushner, Peter J

; APPLICANT: Apriletti, James W

; APPLICANT: West, Brian

TITLE OF INVENTION: Nuclear Receptor Ligands and Ligand

NUMBER OF SEQUENCES: 16

CORRESPONDENCE ADDRESS:

ADDRESSEE: Cooley Godward

STREET: Five Palo Alto Square, 3000 El Camino Real

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94306

COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08764,870

FILING DATE: 13-DEC-1995

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/008, 540

FILING DATE: 13-DEC-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/008, 543

FILING DATE: 13-DEC-1995

RESULT 7  
US-08-980-115-14  
; Sequence 14, Application US/08980115  
; Patent NO. 6266622  
; GENERAL INFORMATION:  
; APPLICANT: Scanlan, Thomas S.  
; APPLICANT: Baxter, John D.  
; APPLICANT: Fletterick, Robert J.  
; APPLICANT: Wagner, Richard L.  
; APPLICANT: Kushner, Peter J.  
; APPLICANT: Apriletti, James W.  
; APPLICANT: West, Brian L.  
; APPLICANT: Shiao, Andrew K.  
; TITLE OF INVENTION: NUCLEAR RECEPTOR LIGANDS AND LIGAND BINDING DOMAINS  
; FILE REFERENCE: UCAL-246702US  
; CURRENT APPLICATION NUMBER: US/08/980,115  
; CURRENT FILING DATE: 1997-11-26  
; EARLIER APPLICATION NUMBER: 08/7764, 870  
; EARLIER FILING DATE: 1996-12-13  
; EARLIER APPLICATION NUMBER: 60/008, 606  
; EARLIER FILING DATE: 1995-12-14  
; EARLIER APPLICATION NUMBER: 60/008, 543  
; EARLIER FILING DATE: 1995-12-13  
; EARLIER APPLICATION NUMBER: 60/008, 540  
; EARLIER FILING DATE: 1995-12-13  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 14  
; LENGTH: 933  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: DOMAIN  
; LOCATION: (659)..(918)  
; OTHER INFORMATION: minimal ligand binding domain

Query Match 18 %; Score 801; DB 4; Length 933;  
Best Local Similarity 29.5%; Pred. No. 4.8e-51;  
Matches 253; Conservative 95; Mismatches 221; Indels 288; Gaps 37;

QY 191 SPSVCSPLNMSSVCSPAG---INSVSIITASCGSFVPHSPRTOCT--PLTC--SPNA 241  
Db 20 SPEVGSPL---LGRPAAGPFPGSOTSPDPEVAISPs--LDDLFPRPCOGQDPSD 71  
Db 20 SPEVGSPL---LGRPAAGPFPGSOTSPDPEVAISPs--LDDLFPRPCOGQDPSD 71

RESULT 8  
5223606-6  
; Patent No. 5223606  
; APPLICANT: BLAUDIN DE THE, HUGHES; MARCHIO, AGNES; TIOLAIS,  
; PIERRE; DEEAN, ANNE  
; TITLE OF INVENTION: STEROID/THYROID HORMONE RECEPTOR-RELATED  
; PROTEIN INAPPROPRIATELY EXPRESSED IN HUMAN HEPATOCELLULAR CARCINOMA  
; NUMBER OF SEQUENCES: 11  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/134,130  
; FILING DATE: 17-DEC-1987  
; PRIOR APPLICATION DATA:  
; SEQ ID NO: 6  
; LENGTH: 363  
; 5223606-6

Query Match 16.6%; Score 732.5; DB 6; Length 363;  
Best Local Similarity 57.0%; Pred. No. 1.4e-46;  
Matches 138; Conservative 37; Mismatches 46; Indels 21; Gaps 5;

QY 286 SSPNPNVTLRSSVSPANINNSRCSYSS-----PSNNNRNSTLSSPAASTVGSCICSP 336  
Db 122 SGPG----QSPQSPPA----CEVTSSWCLFGPELPED-----PPAPAPATORVLS 163  
QY 337 VNNASVYTASGTSAGSSTLRDWP---SPTQ-----EKGAEVFP---KTE 378  
Db 164 LMSR---SGCKYGDSSGTAAHKVLPRLSPAROLLSPASESPHWGAPVKSPQAAVE 222  
Db 1 CLJCGDEPASGCHYGLTCGSCKVFRRAMEGOHNYLCAGRNDVICWKIRRNCPACRLR 60  
QY 603 CHVCGDRASGCHYGVWTGSCCKVFRRAMEGOHNYLCAGRNDVICWKIRRNCPACRLQ 662  
Db 61 CQQAGMVLGGRKFKEKVR-VMRADAVALFAPVGIPNES--ORIF----SPSOEIQ 112  
QY 723 LYVQLSITISRALTPSPMVILENTEPETVAGDSKDTAENLSTLNRLAGKOMIYVK 782  
Db 113 LIPPL-----INLLMSIEPDVYAGHDNKTDFDTSSLTSILSNTSOLBROLQSVK 161

Db 220 RE 221

QY 843 RE 844

Db 342 YKSGALDEAAAYOSRDYINPFLAAGPPPPPPPHARIKLENPLDYGSAWAAAOCR 401

Db 504 .....-PEASIPSSATV.....

Db 402 YGLASLHAGAAAGPGGSPSAAASSWHLSRQDQFQ-.....-DGDSYY .....- 503

QY 488 -----

Db 517 CVSEMPWMDSYSGPYGDMRLTARDHVLPIFYF-.....-POKICL 559

Db 515 ---GVNSQGS---EHYRIGAQTSILSRARDQFQ-.....-HLSSFP-PVNT 555

Db 462 GGGGGGGGEALAWAPGYTRPQGL-.....-AQESEFTAPPWYPGMWSVPYPPT 516

QY 556 LVES---WKS---HGD---LSSRSDCPYPLEYIPEVNSSTLRSVSTGSSRSPSKCL 604

Db 560 ICDEASCHYGAUTCGSCCKVFRKAEGKOKVLCASNRCTIDKFRKRNCPSCLRKY 619

QY 605 VCGDEASCHYGVTCGSCCKVFRKAEGKOKVLCAGRNDCLIDKIRKNCPACRLQCL 664

Db 665 QAGMNGLGARKSKKLKGKIHTEOPQQOOPPPPPPPSSPEEGTYIAPAKEPSVNTALY 724

Db 620 EAGMTLGARKKKKGNLK-LQESEASS-.....-TTSPTEET-.....- 655

QY 725 POLSTISR---ALTPSPVMNLEIPEPEVYAGDVDSKBDTAENLSTLNRAKGQMTV 780

Db 656 -OKLTIVSHEGYFCQPFILNVLEIAEPGVWCAGHDNNQPSFAALLSLNELGERQLVHV 714

QY 781 VKWAKVKGFKNPLEDQITLQYSWMCISLSSFAWSRSKHTNSQFLYFADLVNE 837

Db 715 VKWAKALPGFRNLHDDQMAVIQYSWMQLMVFAMGRSFVNNSRMLYFADLVNE 771

RESULT 9

US-09-041-886-11

; Sequence 11, Application US/09041886

Patent No. 6235872

GENERAL INFORMATION:

APPLICANT: Rabizadeh, Dale E.

APPLICANT: Sharroo

TITLE OF INVENTION: Proapoptotic Peptides, Dependence

TITLE OF INVENTION: Polypeptides and Methods of Use

NUMBER OF SEQUENCES: 72

CORRESPONDENCE ADDRESS:

ADDRESSEE: Campbell & Flores LLP

STREET: 4370 La Jolla Village Drive, Suite 700

CITY: San Diego

STATE: California

ZIP: 92122

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/041,886

APPLICATION NUMBER: US/09/041,886

FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Campbell, Kathryn A.

REGISTRATION NUMBER: 31,815

REFERENCE/DOCKET NUMBER: P-LJ 2626

TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 535-9001

TELEFAX: (619) 535-8949

INFORMATION FOR SSO ID NO: 11:

SEQUENCE CHARACTERISTICS:

LENGTH: 918 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-041-886-11.

Query Match 16.4%; Score 726; DB 4; Length 918;

Best Local Similarity 29.5%; Pred. No. 1.7e-45; Mismatches 19%; Indels 272; Gaps 31;

Matches 229; Conservative 79; MisMatches 19%; Indels 272; Gaps 31;

Qy 238 SPNAENGRRSHSPAHASNVGSPPLSSPKSMKSSISPPSHCSVKSPVSPNNVTLRSSV 297

Db 90 SPOAHRHRPTGYL-----VLDQEQQP-SOPOSALBCHPERGCVP-----GAVAASK 137

Qy 298 SSPANTINNSRSVSSPSNTNRSTLSSPAASTVGSIICSPVNNAFSYTAGTSAGSSTLRD 357

Db 138 GLRQQL-----PAPDDED-----SAAPSLN-SLIGP-----TFPGLSSCSDLKD 177

Qy 358 VVPSPDHQEKGAQEVPPKTEVEASISNGVQLNIVQYTKPEPDGAFSSS----CLGGN 414

Db 178 ILSEASTMQLQQ----QEAVESEGSSGRA-----REASGAPTSSKDNVYGGT 223

Qy 415 SKINSDS-----SFSPVPIKESTKHSCTNSFKGK-----PTVAPFP----- 451

Db 224 STISDNAKELKAVAVSMSGMIGVEALEHLSGPQQLRGDCMYAPLLGVPPAVRPTCAPLAE 283

Db 452 ---FMGDSYISFMDDKDIYISLGLGPPWFGDFG -- -NCEGS----- 487

RESULT 10

5223606-7

Patent No. 5223606

; Patent No. 5223606

; APPLICANT: BLAUDIN DE THE, HUGHES; MARCHIO, AGNES; TIOLLAIS, PIERRE-DEJEAN, ANNE

; TITLE OF INVENTION: STEROID/THYROID HORMONE RECEPTOR RELATED PROTEIN INAPPROPRIATELY EXPRESSED IN HUMAN HEPATOCELLULAR CARCINOMA

; NUMBER OF SEQUENCES: 11

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/134,130

; FILING DATE: 17-DEC-1987

; PRIOR APPLICATION DATA:

; SEQ ID NO:7:

; LENGTH: 356

5223606-7

Query Match 16.1%; Score 713.5; DB 6; Length 356;

Best Local Similarity 60.0%; Pred. No. 3.6e-45; Mismatches 45; Indels 25; Gaps 4;

Matches 141; Conservative 24; MisMatches 45; Indels 25; Gaps 4;

Qy 603 CLVCGDEASGCHGVWTGSCCKVFFKRAVEQHNYLCAGRNDCLIDKIRKNCPACRLQK 662

Db 1 CLVCSDEASGCHGVLTGSCCKVFFKRAVEQHNYLCAGRNDCLIDKIRKNCPACRYK 60

Qy 663 CLOAGMMGARKSKKLKGKKGIBEQPQQQQPPPPQQSPSEGTYIAPAKEPSVNTA 722

Db 61 CLOAGMMNLREAKTRK--KTRK----QQTGTVSOETSENPGNKTIUPATLPO--- 107

Qy 723 LVPQLTISRALTPSPWMLNLEPPEVYAGYISSKPTAENLJSLNLAGKOMIQVK 782

Db 108 -----LPTPLVSLLEVIEPEPVLYAGTDSSVPDSTWRIMTTLNMGGRVIAAV 156

Qy 783 WAKVLPGFKNPLDEDQITLQYSWMCISLSSFAWSRSKHTNSQFLYFADLVNE 837

Db 157 WAKAIPGFRNLHDDQNTLQYSWMFLMA-ALGWSYROSSANLCPAPDLINE 210



Db 245 LHVVKWAKALPGFRNLHVDDQMAVIQYSWMGLMVFAMGWRSPFTNVNSRMLIFAPDLVFN 304  
 Qy 837 E 837  
 Db 305 E 305

RESULT 13  
 US-08-764-870-12  
 ; Sequence 12, Application US/08764870  
 ; Patent No. 6236946

GENERAL INFORMATION:  
 APPLICANT: Scanlan, Thomas S.  
 APPLICANT: Baxter, John D.  
 APPLICANT: Fletterick, Robert J.  
 APPLICANT: Wagner, Richard L.  
 APPLICANT: Kushner, Peter J.  
 APPLICANT: Apilletti, James W.  
 APPLICANT: West, Brian

TITLE OF INVENTION: Nuclear Receptor Ligands and Ligand  
 NUMBER OF SEQUENCES: 16

CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Cooley Godward  
 STREET: Five Palo Alto Square, 3000 El Camino Real  
 CITY: Palo Alto  
 STATE: CA  
 COUNTRY: USA  
 ZIP: 94106

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/764,870  
 FILING DATE: 13-DEC-1996  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: US 60/008,543  
 FILING DATE: 13-DEC-1995  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: US 60/008,540  
 FILING DATE: 14-DEC-1995  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Nakamura, Jackie N  
 REGISTRATION NUMBER: 35,966  
 REFERENCE/DOCKET NUMBER: UCAL-246/01US  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (650)843-5000

SEQUENCE CHARACTERISTICS:  
 LENGTH: 595 amino acids  
 TYPE: amino acid  
 STRANDEDNESS:  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-764-870-12

RESULT 14  
 US-08-980-115-12  
 ; Sequence 12, Application US/08980115  
 ; Patent No. 6266622

GENERAL INFORMATION:  
 APPLICANT: Scanlan, Thomas S.  
 APPLICANT: Baxter, John D.  
 APPLICANT: Fletterick, Robert J.  
 APPLICANT: Kushner, Peter J.  
 APPLICANT: Apilletti, James W.  
 APPLICANT: West, Brian L.  
 APPLICANT: Shiao, Andrew K.

TITLE OF INVENTION: NUCLEAR RECEPTOR LIGANDS AND LIGAND BINDING DOMAINS  
 FILE REFERENCE: UCAL-246/02US

CURRENT APPLICATION NUMBER: US/08/980,115  
 CURRENT FILING DATE: 1997-11-26  
 EARLIER APPLICATION NUMBER: 08/764,870  
 EARLIER FILING DATE: 1995-12-13  
 EARLIER APPLICATION NUMBER: 60/008,606  
 EARLIER FILING DATE: 1995-12-14  
 EARLIER APPLICATION NUMBER: 60/008,543  
 EARLIER FILING DATE: 1995-12-13  
 EARLIER APPLICATION NUMBER: 60/008,540  
 EARLIER FILING DATE: 1995-12-13  
 NUMBER OF SEQ ID NOS: 17  
 SOFTWARE: Patentin Ver. 2.0  
 SEQ ID NO 12  
 LENGTH: 595  
 TYPE: PRT  
 FEATURE:  
 NAME/KEY: DOMAIN  
 LOCATION: (287)-(549)  
 OTHER INFORMATION: minimal ligand binding domain  
 US-08-980-115-12

Query Match 10.1%; Score 445.5; DB 4; Length 595;  
 Best Local Similarity 28.2%; Pred. No. 6.1e-25; Gaps 13;  
 Matches 116; Conservative 68; Mismatches 120; Indels 107; Gaps 13;

Qy 497 PDDGSVYPEASIPSSAIV---GVNSGGQSTHYRGAQGTISLSRSARDQSFQHLSFPP 552  
 Qy 553 VNLVLS-----WKSHD----LSSRSRDGYVLE----YIPEN---- 583  
 Qy 553 VNLVLS-----WKSHD----LSSRSRDGYVLE----YIPEN---- 583  
 Qy 100 INSVSPSPLMLHPPOLSPLOPHGQCVPYLENPSGCVTREAGPFAVRPNSDNRRQ 159

Db 100 LNSVSPSPLMLHPPOLSPLOPHGQCVPYLENPSGCVTREAGPFAVRPNSDNRRQ 159  
 Qy 584 -----VSSSTIRSVSGSSRSRSPSKICLVCGDEASGHYGVTCGSSCKVFRAVECHNY 637  
 Db 160 GGRERLASTNDKGSMAMESAKETRYCVCNDYASYGHYHGWSCEGCKAFKRSI0HNDY 219  
 Qy 638 LCAGRNDCIDIKIRRNCOPACRLQCLQAGMNLGA-RKSKLKGKTHESOPQQQOPP 696  
 Db 220 MCPATNOCTIDKNRKSOCARLRKCYEVGMKGGTRDKRGGRMLK-HKQ----- 270  
 Qy 697 PPPPPSPEEGTYIAFAKERSVNTALVPQJSTISRA-LITPSPVAV----- 741  
 Db 271 -----RDIDGEGRGEVGSSAGD-----MRAANLMPSPIMKRSKNSLALS 311  
 Qy 742 -----LENIEPEIIVYAGDSSKPTAENIJLSTNLAGKOMIQVKAVALVLPGFKNLP 794  
 Db 312 ADQMVSAALLDAEPPILVSEYDPTRPSEASMSGGLNLTADRELVHMWNWAKRVPGFDLT 371  
 Qy 795 LEDQITLQYSNCCLSFAALSURSYKHTNSOFLYFADLVLNELLARVREG 845  
 Db 372 LHDQVHLLCAWLEILMIGLWVRSMEHPGK - LLFAPNLLDRNQSGKCVEG 420

QY 584 -----VSISLUKVSVTSGSRSKRIEKLUVGEGRSCLL-----  
 Db 160 GGRERLASTNDKGSMAMESAKETRYCAVNDYASGYHYGVWSCEGCKAFKFKRSI0GHND  
 QY 638 LCAGRNPCIDTRRKNCAPCRLOQCLQAGMNLGA-RKSKKIGLKGTHEEQPOQQOQP  
 Db 220 MCPATNQCTIDKNRKSCQACLRKCTEVGMKGGIRKDQRGGMLK-HKRO-----  
 QY 697 PPPPPQSPEEGTYIAPAKERSNTALVPOLSTIRA-LTPSPVM-----  
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 Db 312 ADQWMSAIIADAEPPILYSEYDPTPFSASMMGLLTNLADRELVHMINAWKRVPGFVLD  
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 Db 372 LHDQVHLLECAWLEILMIGLWWSMHEPKU-LLFAPNLLDRNQGCVEG 420

RESULT 15  
US-08-836-620A-17  
Sequence 17, Application US/08836620A  
Patent No. 598710  
GENERAL INFORMATION:  
APPLICANT:  
TITLE OF INVENTION: Orphan receptor  
NUMBER OF SEQUENCES: 19  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/0336,620A  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/EP96/03933  
FILING DATE:  
APPLICATION NUMBER: GB 9518272.1  
FILING DATE: 08-SEP-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9605550.4  
FILING DATE: 15-MAR-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9607532.0  
FILING DATE: 11-APR-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9609576.5  
FILING DATE: 08-MAY-1996  
INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 591 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
US-08-836-620A-17

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GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

## OM protein - protein search, using SW model.

Run on: September 13, 2002, 10:15:56 : Search time 36.28 seconds

(without alignments)  
2587.027 Million cell updates/sec

Title: US-09-695-293-42

perfect score: 4422

Sequence: 1 METKGYHSLPEGLDMERRWG . . . . . FLYFAPDLVNFELLARVREG 845

## Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : A\_Geneseq\_032802:\*

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2: /SIDS1/gcadata/hold-geneseq/geneseq-emb1/AA1981.DAT:\*

3: /SIDS1/gcadata/hold-geneseq/geneseq-emb1/AA1982.DAT:\*

4: /SIDS1/gcadata/hold-geneseq/geneseq-emb1/AA1983.DAT:\*

5: /SIDS1/gcadata/hold-geneseq/geneseq-emb1/AA1984.DAT:\*

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8: /SIDS1/gcadata/hold-geneseq/geneseq-emb1/AA1987.DAT:\*

9: /SIDS1/gcadata/hold-geneseq/geneseq-emb1/AA1988.DAT:\*

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11: /SIDS1/gcadata/hold-geneseq/geneseq-emb1/AA1990.DAT:\*

12: /SIDS1/gcadata/hold-geneseq/geneseq-emb1/AA1991.DAT:\*

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14: /SIDS1/gcadata/hold-geneseq/geneseq-emb1/AA1993.DAT:\*

15: /SIDS1/gcadata/hold-geneseq/geneseq-emb1/AA1994.DAT:\*

16: /SIDS1/gcadata/hold-geneseq/geneseq-emb1/AA1995.DAT:\*

17: /SIDS1/gcadata/hold-geneseq/geneseq-emb1/AA1996.DAT:\*

18: /SIDS1/gcadata/hold-geneseq/geneseq-emb1/AA1997.DAT:\*

19: /SIDS1/gcadata/hold-geneseq/geneseq-emb1/AA1998.DAT:\*

20: /SIDS1/gcadata/hold-geneseq/geneseq-emb1/AA1999.DAT:\*

21: /SIDS1/gcadata/hold-geneseq/geneseq-emb1/AA2000.DAT:\*

22: /SIDS1/gcadata/hold-geneseq/geneseq-emb1/AA2001.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score or the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

RESULT : 1

ID AAY21622 standard; protein: 984 AA.

XX AAY21622;

AC AAY21622;

DT 11-AUG-1999 (first entry)

XX DE Ligand binding domain of nuclear receptor hMR.

XX KW Thyroid hormone receptor; aromatic compound; ligand binding domain;

KW alpha-glycerophosphate dehydrogenase; cardiac; obesity; triglyceride;

KW plasma cholesterol; anti-hypertriglyceridaemic; atherosclerosis; GPDH;

KW thyroid hormone replacement therapy; nuclear receptor.

OS Homo sapiens.

PN W092696-A2.

XX PD 03-JUN-1999.

XX PF 25-NOV-1998; 98WO-US25296.

XX PR 26-NOV-1997; 97US-0980115.

XX PA (RECC ) UNIV CALIFORNIA.

XX PI Apriletti JW, Baxter JD, Fletterick RJ, Kushner PJ;

PT Scanlan TS, Shiao AK, Wagner RL, West BL;

XX DR WP1; 1999-357810/30.

XX PT Modulating activity of a thyroid hormone receptor

12	731.5	16.5	919	18	AAW14783	Androgen receptor.
13	731.5	16.5	919	21	AAV78914	Human androgen rec.
14	726	16.4	918	20	AAV3491	Human androgen rec.
15	725.5	16.4	918	10	AAV93109	Human androgen rec.
16	723	16.4	918	12	AAR1223	Human androgen rec.
17	723	16.4	919	10	AAV90996	Human androgen rec.
18	686.5	15.5	952	20	AAV21627	Ligand binding dom.
19	666.5	15.1	630	12	AAR1230	Trp/androgen rec.
20	445.5	10.1	595	20	AAV21626	Ligand binding dom.
21	445.5	10.1	595	22	AAG84505	Human oestrogen rec.
22	445.5	10.1	595	22	AAG84506	Human oestrogen rec.
23	445.5	10.1	595	22	AAE84508	Human oestrogen rec.
24	445.5	10.1	595	22	AAE84509	Human oestrogen rec.
25	445.5	10.1	595	22	AAE84510	Human oestrogen rec.
26	445.5	10.1	595	22	AAE84511	Human oestrogen rec.
27	445.5	10.1	595	22	AAE84512	Human oestrogen rec.
28	445.5	10.1	595	22	AAE84513	Human oestrogen rec.
29	443.5	10.0	595	22	AAE84514	Human oestrogen rec.
30	443.5	10.0	595	22	AAE84515	Human oestrogen rec.
31	442.5	10.0	595	8	AAP70543	Human oestrogen rec.
32	442.5	10.0	595	20	AAV33506	Human oestrogen rec.
33	427.5	9.7	582	22	AAE78227	Leiomys centraricha
34	427	9.7	457	22	AAE61499	Protein encoded by Rat IER beta-4 c/o Protein encoded by Rat oestrogen receptor.
35	423	9.6	423	20	AAU04436	Protein encoded by Rat oestrogen receptor.
36	421.5	9.5	422	22	AAE61498	Protein encoded by Rat oestrogen receptor.
37	420	9.5	414	20	AAW98127	Human oestrogen receptor.
38	417	9.4	530	18	AAW33215	Human oestrogen receptor.
39	417	9.4	530	20	AAW87858	Human oestrogen receptor.
40	417	9.4	530	22	AAE10457	Human Oestrogen receptor.
41	417	9.4	530	22	AAU23732	Human Oestrogen receptor.
42	417	9.4	530	22	AAE60649	Human oestrogen receptor.
43	417	9.4	548	20	AAV07270	Human oestrogen receptor.
44	416	9.4	549	20	AAV04434	Murine MBR beta-1 DNA-binding domain.
45	415	9.4	93	17	AAE90714	

## ALIGNMENTS

RESULT : 1

ID AAY21622 standard; protein: 984 AA.

XX AAY21622;

AC AAY21622;

DT 11-AUG-1999 (first entry)

XX DE Ligand binding domain of nuclear receptor hMR.

XX KW Thyroid hormone receptor; aromatic compound; ligand binding domain;

KW alpha-glycerophosphate dehydrogenase; cardiac; obesity; triglyceride;

KW plasma cholesterol; anti-hypertriglyceridaemic; atherosclerosis; GPDH;

KW thyroid hormone replacement therapy; nuclear receptor.

OS Homo sapiens.

PN W092696-A2.

XX PD 03-JUN-1999.

XX PF 25-NOV-1998; 98WO-US25296.

XX PR 26-NOV-1997; 97US-0980115.

XX PA (RECC ) UNIV CALIFORNIA.

XX PI Apriletti JW, Baxter JD, Fletterick RJ, Kushner PJ;

PT Scanlan TS, Shiao AK, Wagner RL, West BL;

XX DR WP1; 1999-357810/30.

XX PT Modulating activity of a thyroid hormone receptor

Rat androgen recep

PS Disclosure; Fig 3A-R; 447pp; English.

xx  
CC The invention relates to a method for modulating activity of a thyroid  
CC hormone receptor that comprises administration of an aromatic compound  
CC which fits spatially and preferentially into a thyroid hormone ligand  
CC binding domain. The aromatic compound (of a specified formula) can be  
used to increase alpha-glycerophosphate dehydrogenase (GPDH) levels, at  
levels which do not significantly modify cardiac GPDH levels and are  
indicated in the treatment of obesity. The compound also lower total  
CC plasma cholesterol and triglyceride levels and can be used as anti-  
CC hypertriglyceridemic agents. The compound may also be used for treating  
CC atherosclerosis and may be indicated in thyroid hormone replacement  
CC therapy in patients with compromised cardiac function. Sequences  
CC members of the nuclear receptor superfamily.  
xx

SO Sequence 984 AA:

Query	Match	Score	DB	Length
QY	1 METKGYHSLPEGLDMERRWGQVSQAVERSSIGPTERTDENNYMELVNVCVGATPNST	99.2%	20	984;
Db	1 metkgynslpegldmertwgqvsqaverssigtptertdennymelvnvcsgapnsts	100.0%	9	3e-266;
QY	61 QGSSEKEQELLCQLQDNNRPGILSDIKTELESKELSATVAESMGILYMDSYRADYSYE	99.9%	20	984;
Db	61 qgskekqellicqlgnrpgiltsdikteleskeslsvatvaesmgilysmvsrdaysye	99.9%	1	0;
QY	121 QQQQGSMSPAKTYQNVEQLVKFYKGNGHRPSTLSCNTPLRSFMSDGSVNGVMRAI	99.0%	20	984;
Db	121 qqnqgsmspakiyqyneqlvfykgnghrpstlscntplrsfmsdgsvngvmrai	99.0%	1	0;
QY	181 VKSPIMCHEKSPVCSPLNMTSSVCSAGINSVSTASFGSFPRVHSITQTPLTCSNP	99.0%	20	984;
Db	181 vkspmchekspvcspnmlssvcspaginsvsstafsfpsfpvhsitqtpltcsnp	99.0%	1	0;
QY	241 AERGSRSHSPASAENYGSPLSPPSENKSISSPSPHCSCVSKSPVSPSPNNVTLSVSSP	99.0%	20	984;
Db	241 aergrsrshspasnvsplssplssknssisppscvsvpspnvnrlrsssp	99.0%	1	0;
QY	301 ANINNSRCGVSSPNTNRSTLSPAASYGSCISCPVNAFSYTASGTSAGSSTLRDWVP	99.0%	20	984;
Db	301 aninnsrcgvssptnrstlspaasygsciscpvnafstasqtsagsstlrdrvp	99.0%	1	0;
QY	361 SPDTQEKGQAQEVIPPKTEVEVESLISNGTQOLNIWQIKPEDGAFSSCIGGNSKIND	99.0%	20	984;
Db	361 spdtqekgqaevipkteinvescisngtqqnivqikpedgafssciggnksind	99.0%	1	0;
QY	421 SSFSVPIQESTKRISCGHSFKKNPTVNPFPMDGSYFSFMDDKDYSSLGIGPPVGF	99.0%	20	984;
Db	421 ssfsvpikqestkriscgshsfknptvnpfpmdgsyfsfmddkdysslgl9ppvgf	99.0%	1	0;
QY	481 DGNCEGSGGPVGPKQEPDGSYYPEASITSSAATGVNGGGOSHMYRIGAQGTISLSRAR	99.0%	20	984;
Db	481 dgncegsqgpvgpkqepdgssyypeasipsalavgvnsgqgshyriqagqtlslsras	99.0%	1	0;
QY	541 DQSQHLSSFPPTNLVESWKSIQGDLSRRSDGSPVLEYIPEWSSSTLRSVTGSSRPS	99.0%	20	984;
Db	541 dqsqhlssfpptnlvewsksgdlsrrsdgspvleyipewssstlrsvtgsrps	99.0%	1	0;
QY	601 KICIVCGDEASGYGHGVWVGSGKSVFVKRAVEQHONYLCAGRUDCTKIRRNCPACRL	99.0%	20	984;
Db	601 kicivcgdeasgchygvwtcgsckvfkraveeqhnylcagrudctkirrncpacrl	99.0%	1	0;
QY	661 QKCLQAGMNGARKSKKKLGKGHEEQPOQQQPPPPPPQSPPEEGTYIAPAKEPSV	99.0%	20	984;
Db	661 qkclqagmngarkskkklgkgheeqppggppppppsppeegtyiapakepsv	99.0%	1	0;
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Db 721 talvpqlstisraltpspwmleipeivaygdsskpdaenlistlnrlagkqmiv 780  
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Db 781 vkwakvlpgknlpqedqtlqyswmcifalswsryskhtnsqflfapdlvne 837

RESULT 2  
ID AAP80927 standard; protein; 984 AA.  
XX AAP80927;  
AC AAP80927;  
DT 29-DEC-1990 (first entry)

XX Sequence of the human mineralocorticoid receptor (hMR).  
KW Hormone receptor; hormone-binding; transcription activation.  
XX OS Homo sapiens.  
XX PN W08803168-A.  
XX PD 05-MAY-1988.  
XX PF 23-OCT-1987; 87WO-US02782.  
XX PR 20-OCT-1987; 87US-0108471.  
XX PA (SALK ) SALK INST FOR BIOL STUD.  
XX PI Evans RM, Weinberger CA, Hollenberg SM, Giguere V;  
XX DR WPI; 1988-133242/19.  
XX N-PSDB; AAN80920.

PT Recombinant DNA encoding hormone receptors - comprising glucocorticoid, mineralocorticoid, thyroid hormone  
PT and novel hormone receptors  
XX Claim 17; Fig IV-(2)(B)-1 and -2; 243pp; English.  
CC DNAs encoding hormone receptors and the hormone receptors themselves are  
CC claimed. The DNA can be used to make the hormone receptor proteins and  
CC functional modified forms in quantities not previously possible. The  
CC receptor proteins can be used to screen cpd. for receptor-agonist or  
CC receptor-antagonist activity. They can also be used in diagnostic assays.  
XX

Sequence 984 AA:

Query	Match	Score	DB	Length
QY	1 METKGYHSLPEGLDMERRWGQVSQAVERSSIGPTERTDENNYMELVNVCVGATPNST	99.0%	20	984;
Db	1 metkgynslpegldmertwgqvsqaverssigtptertdennymelvnvcsgapnsts	99.0%	9	3e-265;
QY	61 QGSSEKEQELLCQLQDNNRPGILSDIKTELESKELSATVAESMGILYMDSYRADYSYE	99.0%	20	984;
Db	61 qgskekqellicqlgnrpgiltsdikteleskeslsvatvaesmgilysmvsrdaysye	99.0%	1	0;
QY	121 QQQQGSMSPAKTYQNVEQLVKFYKGNGHRPSTLSCNTPLRSFMSDGSVNGVMRAI	99.0%	20	984;
Db	121 qqnqgsmspakiyqyneqlvfykgnghrpstlscntplrsfmsdgsvngvmrai	99.0%	1	0;
QY	181 VKSPIMCHEKSPVCSPLNMTSSVCSAGINSVSTASFGSFPRVHSITQTPLTCSNP	99.0%	20	984;
Db	181 vkspmchekspvcspnmlssvcspaginsvsstafsfpsfpvhsitqtpltcsnp	99.0%	1	0;
QY	241 AERGSRSHSPAHASNYGSPLSPPSISSPHCKSCVSKSPVSPSPNNVTLSVSSP	99.0%	20	984;

DB	301 ANINNSRCVSNSPNTNNRSTLSSPAASTVSGCICSPVNNAFSYTAAGTSAAGSSTLRDWP 360	CC	xx	Claim 24; FIG I-2(1) to (2); 243pp; English.
Db	301 aninnsrcvsnspsntnnrstlsspaastvsgcicspvnnafsytaagtsagsstlravp 360	CC	CC	DNA's encoding hormone receptors and the hormone receptors themselves are claimed. The DNA can be used to make the hormone receptor proteins and functional modified forms in quantities not previously possible. The receptor proteins can be used to screen cpd's for receptor agonist or receptor-antagonist activity. They can also be used in diagnostic assays.
OY	361 SPDTQEKGAEQVPPPKTEEVESAIISNGVTGQLNIVQIKPERDGAFSSCLGNNSKINSD 420	CC	XX	
Db	361 spdtqekgagewpfkpteevesaisnqvtgqgnivqykpepdgatsssciggnsknsd 420	SQ	Sequence 777 AA;	
OY	421 SSFSVVIKQESTKHSGSGTSFKGNPTVNPFPMDGSYFSPMDKDDKYDYLGLGPVPGF 480			
Db	421 ssfsvpkqkfstkhsqsgtsfkgnptvnpfpmdgsyfsmddkydylsqslsqqlqpgf 480			
OY	481 DNGCEGSGFPVGKIQEPPDDGSYYPEASIPSSAIVGANSGGOSFYRIGAQTISLSAR 540			
Db	481 dgncedsgfpvgqikqgpddgsyypeasipssavgnsgqsfhyrigaqgtislsar 540			
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Db	601 kiclvgeadeaschygavtccsvkfvkravghqnyicagendcidiirkncapcr 660			
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OY	721 TALVPOLSTISRALTSPVMVNIENIEPEIIVAGYDSSKPTAENLSTLNRLAGKOMTQV 780			
Db	721 talvpqlstishkaltpspmvnienepeiyagydsskptdaenlsltnrlagkomiq 780			
OY	781 VPKWAKVLPFGKMLPLEDQTTLIOYSWMCSSFLASWYSYKHNSOFLYFAPDLVNE 837			
Db	781 vkwakvlpfgkmlpledqtlqyqswmcslsflaswysykhnsqflfyapdlvne 837			
RESULT 3	AAP80919	ID	Best Local Similarity 35.0%; Pred. No. 3.4e-45;	Query Match 19.4%; Score 856; DB 9; Length 777;
	AAP80919 standard; protein: 777 AA.		Matches 239; Conservative 83; Mismatches 212; Indels 148; Gaps 25;	Matches 239; Conservative 83; Mismatches 212; Indels 148; Gaps 25;
AC	AAP80919;	XX		
XX	29-DEC-1990 (first entry)	DT		
XX	Sequence of the primary protein sequence of human glucocorticoid receptor (hGR).	DE		
XX	Hormone receptor; hormone-binding; transcription activation.	KW		
OS	Homo sapiens.	OS		
PN	W08803168-A.	PN		
XX	05-MAY-1988.	PD		
XX	23-OCT-1987; 87WO-US02782.	PR		
XX	20-OCT-1987; 87US-0108471.	PR		
PA	(SALK ) SALK INST FOR BIOL STUD.	XX		
PI	Evans RM, Weinberger CA, Hollenberg SM, Giguere V;	XX		
DR	WPI: 1988-133242/19.	XX		
N-PSDB; AAN80916.				
PT	Recombinant DNA encoding hormone receptors - comprising glucocorticoid, mineralocorticoid, thyroid hormone and novel hormone receptors	PT		
XX				
RESULT 4	AAW44700	ID	Query Match 19.4%; Score 856; DB 9; Length 777;	Query Match 19.4%; Score 856; DB 9; Length 777;
	AAW44700 standard; Protein: 777 AA.	XX	Matches 239; Conservative 83; Mismatches 212; Indels 148; Gaps 25;	Matches 239; Conservative 83; Mismatches 212; Indels 148; Gaps 25;
AC	AAW44700;	XX		
XX	12-MAY-1998 (first entry)	DT		
XX	Mutant nuclear glucocorticoid receptor 174T.	DE		

XX	Mutant; nuclear glucocorticoid receptor; ligand binding domain;	QY	399 KPEPGDAFESSCLGNISKI--NSDSSFSV-----PIKQESEKHKHSGSGTSFKGNPT 446
KW	Point mutation; site-directed mutagenesis; fusion protein; recombinase;	Db	174 -----tgnsgnvnklytdstfaidqleffsgsgketaewspwsdallidenc 224
KW	bacteriophage PI; gene therapy; recombination; loxp.	PR	447 VNPFPPMDGSYF-----SFMDDKYI--SLSGILGLGPVPGFDGNE 485
OS	Homo sapiens.	FR	225 lspiageddsfilegnsneackpkplpdtkpkikangdvlvsspnvtlpq---kte 279
OS	Synthetic.	Key	FR2745008-A1.
XX	Location/Qualifiers	FH	XX
XX	Key-difference 747	FT	Misc-difference "amino acid replacement from I to T"
XX	(ASRE-) ASSOC DEV RECH EN GENETIQUE MOLECULAIRE.	PR	20-FEB-1996; 96FR-0002060.
XX	Brocard JB, Chambon PH, Gronemeyer H, Metzger D;	PR	20-FEB-1996; 96FR-0002060.
PI	Nicolas JC, Roux S;	DR	WPI; 1997-451186/42.
XX	DR	DR	N-PSPDB; AAV05701.
XX	DNA encoding mutated nuclear glucocorticoid receptor - and vector system for protein expression inducible by synthetic glucocorticoid ligand	PT	DNA encoding mutated nuclear glucocorticoid receptor - and vector system for protein expression inducible by synthetic glucocorticoid ligand
XX	Claim 3; Page 50-53; 92pp; French.	SQ	Claim 3; Page 50-53; 92pp; French.
CC	This is the amino acid sequence of a mutant nuclear glucocorticoid receptor (NGR), especially mutated in the region encoding the ligand binding domain (LBD), such that the activity of the receptor is induced more strongly by a synthetic glucocorticoid ligand than by a natural glucocorticoid ligand. The mutation is a point mutation in the coding sequence (a transition mutation) generated by site-directed mutagenesis. This causes a replacement of the Ile residue at position 747 with a Thr residue. The position lies in the region between helices 11 and 12. The mutant coding sequence is used to generate a fusion protein comprising a protein whose activity is to be regulated by and fused to the NGR sequence. The protein is preferably a recombinase, especially the Cre recombinase from bacteriophage PI (see AAV05702). The sequence encoding the fusion protein, and vectors containing it, are used to treat cells either ex vivo or in vitro for use in gene therapy. Vectors containing and expressing the protein allow the transfer of heterologous genes to the cells, genome by recombinase-directed recombination at loxp sites. By using a mutated LBD, normal physiological levels of the ligand will not induce recombination. This requires an increased level of a synthetic ligand.	CC	This is the amino acid sequence of a mutant nuclear glucocorticoid receptor (NGR), especially mutated in the region encoding the ligand binding domain (LBD), such that the activity of the receptor is induced more strongly by a synthetic glucocorticoid ligand than by a natural glucocorticoid ligand. The mutation is a point mutation in the coding sequence (a transition mutation) generated by site-directed mutagenesis. This causes a replacement of the Ile residue at position 747 with a Thr residue. The position lies in the region between helices 11 and 12. The mutant coding sequence is used to generate a fusion protein comprising a protein whose activity is to be regulated by and fused to the NGR sequence. The protein is preferably a recombinase, especially the Cre recombinase from bacteriophage PI (see AAV05702). The sequence encoding the fusion protein, and vectors containing it, are used to treat cells either ex vivo or in vitro for use in gene therapy. Vectors containing and expressing the protein allow the transfer of heterologous genes to the cells, genome by recombinase-directed recombination at loxp sites. By using a mutated LBD, normal physiological levels of the ligand will not induce recombination. This requires an increased level of a synthetic ligand.
XX	Sequence 777 AA;	SQ	Sequence 777 AA;
XX	Query Match 19.4%; Score 856; DB 18; Length 777; Best Local Similarity 35.0%; Pred. No. 3; 4e-45; Matches 239; Conservative 83; Mismatches 212; Indels 148; Gaps 25;	PR	RESULT 5
QY	248 SHSPAHASNNGSPLSPLSSMKSISSSPSPSHCSVKSPVSSPNVNTRSVSSPANTINNSR 307	ID	AY21623
QY	6 siltbgreenppsvlaqeravmdfyktrrgatkvksassps----lavasqsdskrr 60	ID	AY21623 standard; protein; 777 AA.
Db	308 CSVSPSNNTNRS--TLLSSPAASIVG----SICSPVNNAFSYTAGS--TSAGSSTLR 356	AC	AY21623:
Db	61 llvdpfkgsvsnaqpdslsmlgnyetekvymgnalgpqqqqlsgetdk 120	DT	11-AUG-1999 (first entry)
Db	121 lleesianlnirstevpenkkassavsaaptekefpktisndvssseqnlkqg---- 173	XX	Ligand binding domain of nuclear receptor hGR.
XX	Homo sapiens.	XX	Thyroid hormone receptor; aromatic compound; ligand binding domain; alpha-glycerophosphate dehydrogenase; cordiac; obesity; tri-lyceride; plasma cholesterol; anti-hypertensive; diacidaic; atherosclerosis; GPPH; thyroid hormone replacement therapy; nuclear receptor.
XX	OS	PN	WO926966-A2.
XX	PD	03-JUN-1999.	03-JUN-1999.
XX	PR	25-NOV-1998; 98WO-US25296.	PR
XX	PR	26-NOV-1997; 97US-0980115.	PR
XX	PA	(REGC ) UNIV CALIFORNIA.	XX
XX	PI	Apriletti JW, Baxter JD, Fletterick RJ, Kushner PJ;	PI
XX	PI	Scanlan TS, Shiao AK, Wagner RL, West BL;	PI
XX	DR	WPI; 1999-357810/30.	DR
XX	PT	Modulating activity of a thyroid hormone receptor	PT
PS	Disclosure; Fig 3A; R; 447pp; English.	PS	Disclosure; Fig 3A; R; 447pp; English.

The invention relates to a method for modulating activity of a thyroid hormone receptor that comprises administration of an aromatic compound which fits spatially and preferentially into a thyroid hormone ligand binding domain. The aromatic compound (of a specified formula) can be used to increase aliphatic-glycerophosphate dehydrogenase (GPDH) levels at levels which do not significantly modify cardiac GPDH levels and are indicated in the treatment of obesity. The compound also lowers total plasma cholesterol and triglyceride levels and can be used as anti-hypertriglyceridaemic agents. The compound may also be used for treating atherosclerosis and may be indicated in thyroid hormone replacement therapy in patients with compromised cardiac function. Sequences of members of the nuclear receptor superfamily.

xx  
SQ Sequence 777 AA;

Query Match 19.4%; Score 856; DB 20; Length 777;  
 Best Local Similarity 35.0%; Pred. No. 3.4e-45;  
 Matches 239; Conservative 83; Mismatches 212; Indels 148; Gaps 25

QY 248 SHSPAHASNVGSPPLSSPLLSMKSIISSPPSHCSVKSPVSPVNNTLRSVSSPANINR 307

Db 6 s1tpgreenppsvlaquerdvdmyfktirrgatkvksassps-----lavasqdsdkqr 60  
Ov 308 CSVSSPWNNNRS---TISPAASWG-----STCSVWNNTSYTAC---TSCSSTP 356

Db  
61 livdtpkgsnsnqpdkskavslsmglyngetekvngmlngfpqqqsisgetdlk 120

Qy 399 KPEPDGFSSCLGGNSKI--NSDSSFV-----PIKQESTKHSCTGTSFKGNPT 446

Db 174 - - - - - tgtnqgnvkyttdqstdilqlefssgspktnespwrsdlidenc 224

Qy 447 VNFFPFMMSYF-----SFMDDKDYY--SLSGIGPPVPCFRDGNC 485  
| : | : | : | : | : | : | : | : | : | : | : | : | : | : |  
Db 225 Isplageddsfillegnsnackpllpdkkkidangolvisspsntlpqv-----kte 279

QY 486 GSGF---PVGIKQEPDDGSVYPPEASIPSSAIVG-----VNSGGOSFHRYRIGA 529

Db 280 kedfieldpgvjkqe-kigtvycqasfpganilignkmsaisvhgvstsggmyhyam - 336  
OY 530 OCTISLSRASDOSFOHLLSEPPWNIVIWEW --KSICG--SSRRSRYGPVLETPRNW 584

Db 337 -ntaslsqg-qdqk-pifnvippvgwenvrcqggdnltsglnfpgrtvfsqy 393

NYLCAGRNDCIIDKIRRKNCAPCROLQCLQGMNLARKSKKGKLGIHQQQQQPP 695  
OY

Db 550 ssvpdstwimttinmlsgrrqviaavkwakalpgrfnnlhddqmtlqyswmfimafalg 609  
Oy 816 WISYKHTNQSQFLYPAPDLVNE 837

Db 610 wrsyqssanllcfapdline 631

RESULT 6  
AAW17789 standard; Protein; 1070 AA.  
ID AAW17789

Db	403	qgqqlglssgetdfilleesi-----	XX	18-FEB-2000; 2000MO-EP01368.
Qy	182	KSPIMCERKSPVGSPLNTSSVSPAGINSVSSSTASRGSPFPHSPITQGTPITCSPNA	PR	XX
Db	423	-----anhrstsve---npksttsatlgcatptekerfk-thdasseq	PR	19-FEB-1999; 99DB-1007099.
Qy	242	ENRSRSHSPAHASNVGSLSPSSMKSISSPSPHCSVKSVSSPNNVTLSVSSPA	PA	XX
Db	464	qnrsqt----gnggsvklypdqsfalk-dletsagsbskdtnespwsldide	PA	(THER-) THERAGENE BIOMEDICAL LAB GMBH.
Qy	302	NINNSRCVSSP---SNNNRSTLSSPAASTVGSCVNNAAFSITASGISAGSSILRD	PI	Hauseer-funke C;
Db	518	nllsplageddpfilleagned-----ckp-----	XX	WPI: 2000-549273/50.
Qy	358	VVPSPDTQERGAQAVPPKTEEVESAISNGVTGOLNTIVQYIKPFPDGAFSSCLGGNSKI	DR	DR-N-BDB; AA53851.
Db	543	-lilpdtk-----pkidt-----	XX	
Qy	418	NSDSFSVSP-IKQGSTKHSCEGTSFKGNPTVNPFPMGSYSEFMDDKYDYLGLPP	PT	
Db	561	sspsvalpalqvtek-----ddafielc-----	PT	
Qy	477	VPGDGNCNGCSGFVPGIKBPDGSSYPERASIFSAIVG-----VNSGQSFHIV	XX	
Db	583	tpgv-----ike-pe-kigpvyqcasfqsgtgnmksaisvhgystsgqmhy	PS	
Qy	526	RIGAQGTISLRSARDQSFQHLSSFPVNLVESWK-----SHGDL-----SRR	XX	
Db	630	dm--ntaslsqg-qdqk-pfvnippipvgvsgedsls-----galnprgrf	XX	
Db	571	SDGVPVLEYTPENTSSSTRSVRSRSGRSKICVCGDASGCHGVVTCGSCUVFFKRA	CC	New nucleic acid constructs are described which comprise an hormone responsive element (RE) and a transgene (T). Alternatively the nucleic acid construct, comprises at least one HRE and a transgene, where one of the HREs is not functionally linked to the transgene. The constructs can be used to up-regulate or down-regulate target genes and for the delivery of vaccines. The constructs preferably comprise a transgene which encodes a protein which is lacking in a variety of genetic disorders or involved in conditions related inappropriately to hormones, for example hormone-dependent cancers such as breast, ovarian, and endometrial cancers and prostate cancer. The transgene may also be used to replace a defective gene resulting in such genetic disorders as haemophilia, von Willebrand disease, and cystic fibrosis. Vectors comprising these constructs where the transgene is human clotting factor IX can be used for treating blood clotting disorders such as haemophilia A or B on administration to an organism or to a cellular system. The constructs have applications in gene therapy for treating haemophilia when the transgene encodes a clotting factor such as clotting factor IX. The advantage of this system is that the hormone-hormone receptor complex contains a hormone receptor that becomes activated after binding of its specific hormone. The hormone receptor in the activated state is able to recognise and bind to its specific hormone responsive element. The presence of the hormone responsive element on the nucleic acid carrying a transgene encourages binding of a hormone-hormone receptor complex. Thus the activated hormone receptor acts as a link between the nucleic acid carrying the transgene and the hormone known to interact with the cell membrane.
Qy	685	sngysspgmrpdvssppssaaqgp--ppklcvcsdeasgchygvtcgscvfkra	CC	
Qy	631	VEGHNYLCAGRNIDCIKIRRKPCACRLQKCIQAGMNLGARSKKGKLUKGHEEQQ	CC	
Db	743	veghnylcegrncoidekkirrkpcacryrkclqagmnllearktkk--kikgqataq	CC	
Qy	691	QQPPPPPQQSPREPGTVIAPKEPSVNTALPOLSTISRAJTPSPVWLEPEVY	CC	
Db	801	vsq-----dtseenpnktivlpq-----1ptplvilevepevi	CC	
Qy	751	YAGINSSKKPTAENULSTLNRLASKOMIQVVKWAKVLPGFKNLDEDQITLIQYSWMCLS	CC	
Db	838	yagjdsvvpsdawarinttlnmlgqriavkawakailgrrnlhdqntlqyswmflm	CC	
Qy	811	SFLASWSRYXHTNSQFLYFAPDLVNE 837	CC	
Db	898	:         : ::       :     afalgwrsyqssgnlcfapdlne 924	CC	
RESULT	7	Sequence 933 AA:	XX	
AYY97297	ID	Query Match 18.2%; Score 806; DB 21; Length 933; Best Local Similarity 29.1%; Pred. No. 5.8e-42; Matches 248; Conservative 95; Mismatches 231; Indels 278; Gaps 33;	AYY97297 standard; Protein: 933 AA.	
XX	AYY97297;	Matches 248; Conservative 95; Mismatches 231; Indels 278; Gaps 33;		
XX	03-JAN-2001 (first entry)	Qy 191 SPSVESPMLNNSVSPAG---INVSUTATSGSPFPHSPITQGTP---PLTC---SINA	241	
DT	XX	Db 20 speyqsp1----lerpaagpfqpsqtsatlpepsi	71	
XX	DE Human progesterone receptor B-form.	Qy 242 EN-----RSRSHSPAHASNVGSPLSSP-----LSSMKSISSPSHCSVKSPV	285	
XX	XX	Db 72 ektqdqqlsldvegaysraatrgaggsppeskadglsvidtlap-----121		
XX	Recombinant DNA; gene therapy; hormone responsive element; transgene; HRE; haemophilia; clotting factor IX; vaccine; regulation; breast cancer; ovarian cancer; prostate cancer; von Willebrand disease; cystic fibrosis; hormone; receptor; human; blood.	Qy 286 SSPNNVTLSRSSVSSANINNSRCVSS-----PSWNNTLSSPAASTVGSCSP	336	
XX	OS Homo sapiens.	Db 122 sqpq---sqqsppa-----cevtswclfgpelped-----ppaatqrvisp	163	
XX	PN WO200049147-A1.	Qy 337 VNNAFSYTAASSTASLWDWP---SPNQ-----EKAQEVEPPKKEEVVA	383	
PD	24-AUG-2000.	Db 164 lmsr sgckvqgdssqtaahkvlpqlgsparqlipasesphwgapvprspqaaeve	222	
PD		Qy 384 ISNGVIGOLNIYVOYKPEPPGAFFSSCLGGNSKI-----NSDSSFSV-----426	223	
PD		Db eedgseeseeagplikgpralgyaaaggaaavppgaagvalvpkeedrsaprval	282	







Db	209	-eatgapssksdysyqgnstl-sdsakelckavasvsmg-gvealehlspgeqirgdcmv	265
QY	445	-----PTVNFP-----FMDGSYFSFMDKDYSLSGTILGPVPGFFGNCES	486
Db	266	asllggppavrptpcplaekglslideggpkgtteayssfsfkqyakylegeslgcq	325
QY	487	S---GFPVGKIQPFDGGSYPEASIPSSAIVNVNCGSF-----HYRIG	528
		ssagssgttelpsslyksqgavdeaay qnrdynfnplalsgpphpptphpharik	384
Db	529	AQCTISLS-----RSARDQSQHLSFRPPNTLVEWSKS-----HGDL--	566
QY	385	: : : : leupldygssawaaaqcrqyglashggsvarpstsgspatassswhtiftaaeqqly 444	
QY	567	-----SSRRSDSCPVILEY----IPENVS-----STLRS	591
Db	445	pgggggsspsdaqpvapqytrppqglasqeqdfssasevwypqgyvrpypscvs	504
QY	592	-----VETGSSR-----PSKICLWCGDEASGCHXKVVTGCKY	625
Db	505	empwmeynsgpygdmildstrdhvlpidyyfppqkctilicgdeasgchqyaltcgcky	564
QY	626	FFKRAVECQHNTLCAGRNDCIDKIRKNCPACRLQKCLQAGMNNGARKSKKLKGKIGH	685
Db	565	ffkraaegkqkyicasrndctidkrknccpscrirkcyeagmtlgarkllkglnk-1q	623
QY	586	EEOPQQOOPPPPPPPOSPEEGTYLAPAKERSVNTALVPQLISTR--ALTSPVMM	741
Db	624	ee-----gennsagsgpteds-----qkmtyvhriegyecqiplinv	659
QY	742	LLENTEPEVYAGIDSSKKDTAENLNLSTLNLAGKOMIQVVKAVVLPGFKNPLDQITL	801
Db	660	lealepgvvcaghodnnqpsafallissinegerqivhvkvkawakalpgfrnlhvddqimav	719
QY	802	IQYSWAMCLSSFALSWSRSKHTNSQFLYFAPDLVNE	837
Db	720	ieysswmgimvfangwrsftvnvsrmlyfadlvin	755
RESULT	12		
ID	AAW14783		
ID	AAW14783	standard; Protein: 919 AA.	
AC	XX		
XX	AAW14783;		
XX	DT	22-JUN-1997 (first entry)	
XX	DE	Androgen receptor.	
XX	KW	Androgen receptor; acidic fibroblast growth factor; aFGF; antisense; benign prostatic hyperplasia; prostate cancer; therapy.	
OS	Hom sapiens.		
XX	PN	WO9711170-A1.	
XX	PD	27-MAR-1997.	
XX	PF	20-SEP-1996; 96WO-US15081.	
XX	PR	20-SEP-1995; 95US-0004018.	
XX	PA	(WORC-) WORCESTER FOUND BIOMEDICAL RES.	
PI	Zamecnik PA;		
XX	DR	WPI: 1997-202479/18.	
DR	N-P5DB; AAT63407.		
PT	Oligonucleotide(s) antisense to human androgen receptor and acidic FGF genes - used to inhibit gene expression, for the treatment of benign prostatic hyperplasia		

XX  
PS  
XX  
CC Human androgen receptor (AAW14783) binds testosterone and, acting at the transcriptional level, regulates the growth of normal prostatic cells. Antisense oligonucleotides (see also AAT63200, AAT63404-05) based on an androgen receptor cDNA clone (see also AAT63407) can be used to prevent androgen receptor gene expression, thereby inhibiting the growth or survival of prostatic cells for the treatment of benign prostatic hyperplasia and prostate cancer.  
CC  
XX  
SQ Sequence 919 AA;





Search completed: September 13, 2002, 10:17:42  
Job time: 106 sec

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## OM protein - protein search, using sw model

Run on: September 13, 2002, 10:15:56 : Search time 25.39 Seconds

(without alignments) 3197.932 Million cell updates/sec

Title: US-09-695-293-42  
Perfect score: 4422  
Sequence: 1 METKGHSLPEGLDNERWG... . . . . . FLYFAPDLVENVELLARVREG 845

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched:

283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Maximum Match 0%

Listing first 45 summaries

Database :

PIR\_711,\*  
1: pir1,\*  
2: pir2,\*  
3: pir3,\*  
4: pir4,\*

Pred No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	4385	99.2	984	A29513 mineralocorticoid receptor - human
2	3919.5	88.6	981	A29513 mineralocorticoid receptor - human
3	865	19.6	771	A29513 mineralocorticoid receptor - human
4	856	19.4	54407	A29513 mineralocorticoid receptor - human
5	855	19.4	742	A29513 mineralocorticoid receptor - human
6	836	19.4	777	A29513 mineralocorticoid receptor - human
7	845.5	19.1	775	A29513 mineralocorticoid receptor - human
8	842	19.0	783	A29513 mineralocorticoid receptor - human
9	823	18.6	923	A29513 mineralocorticoid receptor - human
10	814.5	18.4	578	A29513 mineralocorticoid receptor - human
11	805	18.2	786	A29513 mineralocorticoid receptor - human
12	804	18.2	923	A29513 mineralocorticoid receptor - human
13	801	18.1	933	A29513 mineralocorticoid receptor - human
14	800	18.1	930	A29513 mineralocorticoid receptor - human
15	789	17.2	2	A29513 mineralocorticoid receptor - human
16	758.5	17.2	902	A29513 mineralocorticoid receptor - human
17	731.5	16.5	919	A29513 mineralocorticoid receptor - human
18	730.5	16.5	910	A29513 mineralocorticoid receptor - human
19	730.5	16.5	911	A29513 mineralocorticoid receptor - human
20	718	16.2	848	A29513 mineralocorticoid receptor - human
21	644.5	14.6	344	A29513 mineralocorticoid receptor - human
22	461.5	10.4	1451330	A29513 mineralocorticoid receptor - human
23	456.5	10.3	589	A29513 mineralocorticoid receptor - human
24	452.5	10.2	2	A29513 mineralocorticoid receptor - human
25	449.5	10.2	166	A29513 mineralocorticoid receptor - human
26	442.5	10.0	595	A29513 mineralocorticoid receptor - human
27	442.5	10.0	701	A29513 mineralocorticoid receptor - human
28	440.5	10.0	599	A29513 mineralocorticoid receptor - human
29	436	9.9	600	A29513 mineralocorticoid receptor - human

## ALIGNMENTS

30	417	9.4	530	2	JC5939	estrogen receptor
31	404	9.1	477	2	S71400	estrogen receptor
32	398.5	9.0	503	2	JW0045	estrogen receptor
33	395.5	8.9	620	2	T10423	estrogen receptor
34	393.5	8.9	521	2	A29345	estrogen receptor
35	377.5	8.5	701	1	S33709	DHR39-short protein
36	377.5	8.5	808	1	S33708	nuclear steroid/th
37	376	8.5	433	2	B29345	steroid hormone re
38	376	8.5	574	2	A37197	estrogen receptor
39	375.5	8.5	535	2	558224	oestrogen receptor
40	368	8.3	433	2	S58087	estrogen receptor
41	350	7.9	1043	2	T13733	FTRZ-F1 protein - f
42	340	7.7	601	1	ORMSN1	probable hormone r
43	338.5	7.7	598	2	A37251	probable nuclear h
44	338	7.6	628	2	JC2493	neuron derived org
45	335.5	7.6	625	2	S71930	neuron-derived rec





glucocorticoid receptor, beta splice form - human  
 N;Alternate names: hGR  
 C;Species: Homo sapiens (man)  
 C;Date: 04-Dec-1986 #sequence\_revision 04-Dec-1986 #text\_change 21-Jul-2000  
 C;Accession: B93370; B33779; A03247  
 R;Hollenberg, S.M.; Weinberger, C.; Ong, E.S.; Cerelli, G.; Oro, A.; Lebo, R.; Thompson, Nature 318, 635-641, 1995  
 A;Title: Primary structure and expression of a functional human glucocorticoid receptor  
 A;Reference number: A93370; MUID:86092206  
 A;Accession: B93370  
 A;Molecule type: mRNA  
 A;Residues: 1-742 <HOL>  
 A;Cross-references: EMBL:X0348; GB:MI1050; NID:g31681; PIDN:CAA27054.1; PID:g31682  
 R;Encio, I.J.; Detera-Wadleigh, S.D.  
 J. Biol. Chem. 266, 7182-7188, 1991  
 A;Title: The genomic structure of the human glucocorticoid receptor.  
 A;Reference number: A39779; MUID:91201378  
 A;Accession: B93779  
 A;Status: nucleic acid sequence not shown; not compared with conceptual translation  
 A;Molecule type: DNA  
 A;Residues: 385-404; 441-459; 480-498; 573-593; 621-640; 665-685; 718-737 <ENC>  
 A;Cross-references: GB:460597  
 A;Experimental source: placenta  
 R;Weinberger, C.; Hollenberg, S.M.; Rosenfeld, M.G.; Evans, R.M.  
 Nature 318, 670-672, 1985  
 A;Title: Domain structure of human glucocorticoid receptor and its relationship to the vimentin gene  
 A;Reference number: A93373; MUID:86092211  
 A;Contents: annotation; domains  
 C;Comment: Alpha (see PIR:ORHUGA) and beta splice forms differ in their carboxyl-terminal however, it is possible that variant receptors perform tissue-specific functions.  
 C;Genetics:  
 A;Gene: GDB:GRL  
 A;Cross-references: GDB:120017; OMIM:138040  
 A;Map position: 5q31-5q31  
 A;Introns: 395/2; 451/1; 490/1; 583/1; 631/2; 675/1; 727/3  
 A;Note: the first intron occurs before the initiator codon  
 C;Superfamily: glucocorticoid receptor; erbA transforming protein homology/  
 C;Keywords: alternative splicing; DNA binding; nucleus; steroid hormone receptor; transactivator; erbA; transforming protein homology <ERBA>  
 F;412-441/Region: zinc finger cccccc motif  
 F;457-481/Region: zinc finger CCCC motif

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Query Match 19 4%; Score 856; DB 1; Length 742;  
 Best Local Similarity 35.0%; Pred. No. 3.7e-37;  
 Matches 239; Conservative 83; Mismatches 212; Indels 148; Gaps 25;

QY 248 SHSPAHASNVGSPSSPLSSMSKSTSPPSPSHCSVSKRSPVSSPNNYTLRSSVSPANINNSR 307  
 Db 6 SLTPOGREENSSVLAQERGDVMDYKTLRGATKVASSPSS---LAVASOSDSKQR 60

QY 308 CSVSPSNTNRS--TUSSPAATNG---SCSPVNNAFSTASYG--TSAGSST 356  
 Db 61 LLVDPEPKGSVSNAAQPDLSAVAVSMGLYMGTEITVKVMNDLGPFQQGQLSLSSGETIDLK 120

QY 357 DVPS-----PDHQEKAO-----EVFPKTEEVEAISNGVGTQGLNIVQYI 398  
 Db 121 LLEESIANLNRSSTVPPENPKSSAVASAAPTERKEFPKTHSDVSESEQHLKGQ----- 173

QY 399 KPEPDGAFFSSCLGGNSKI - NSSSFSV-----PIQGSTKHSGSGTSFKGNPT 446  
 Db 174 -----TGTTNGNQVNLVYLTDPDASTFDLQDLFSSPGPKENESPWSDLIDENCL 224

QY 447 VNPFPMDSGYF-----SFMDKDY--SLSGIGPPVPGFDGNE 485  
 Db 225 LSPLAGEDDSFLLEGNSNEDCKPILPDKPKIKDNGDLVLSSNSNTLPQV---KTE 219

QY 486 GSGF----PVGIKOPDPDGSYVFAPISSAIVG-----VNPGQSPHYRIGA 529  
 Db 280 KDFELCTPGVQKE-KLGTVYCOASFPGANITIGNKMSAISVHGVTSGQHOMHYDM-- 336

QY 530 QGTLSLSRQDSFOHLSFFFPMVLVESW--KSHGD-LSSRRSDGPVLEKIPENV 584

---

RESULT 6

ORHUGA

N;Alternate names: hGR  
 C;Species: Homo sapiens (man)  
 C;Date: 04-Dec-1986 #sequence\_revision 04-Dec-1986 #text\_change 21-Jul-2000  
 C;Accession: A93370; A93779; 156596; A03246; A32196  
 R;Hollenberg, S.M.; Weinberger, C.; Ong, E.S.; Cerelli, G.; Oro, A.; Lebo, R.; Thompson, Nature 318, 635-641, 1985  
 A;Title: Primary structure and expression of a functional human glucocorticoid receptor.  
 A;Reference number: A93370; MUID:86092206  
 A;Accession: A93370  
 A;Molecule type: mRNA  
 A;Residues: 1-777 <HOL>  
 A;Cross-references: EMBL:X03225; GB:MI10901; NID:g31679; PIDN:CAA26976.1; PID:g31680  
 R;Leclerc, S.; Xie, B.; Roy, R.; Govindan, M.V.  
 J. Biol. Chem. 266, 8711-8719, 1991  
 A;Title: Purification of a human glucocorticoid receptor gene promoter-binding protein  
 A;Reference number: A39837; MUID:1224661  
 A;Accession: A39837  
 A;Molecule type: DNA  
 A;Residues: 1-394 <EC>  
 A;Cross-references: GB:469104; NID:g183605; PIDN:AAA88049.1; PID:g553322  
 R;Encio, I.J.; Detera-Wadleigh, S.D.  
 J. Biol. Chem. 266, 7182-7188, 1991  
 A;Title: The genomic structure of the human glucocorticoid receptor.  
 A;Reference number: A39779  
 A;Molecule type: DNA  
 A;Residues: 385-404; 441-459; 480-498; 573-593; 621-640; 665-685; 718-737 <ENC>  
 A;Cross-references: GB:460597  
 A;Experimental source: placenta  
 R;Weinberger, C.; Hollenberg, S.M.; Rosenfeld, M.G.; Evans, R.M.  
 Nature 318, 670-672, 1985  
 A;Title: Domain structure of human glucocorticoid receptor and its relationship to the vimentin gene  
 A;Reference number: A93373; MUID:86092211  
 A;Contents: annotation; domains  
 R;Dahlman, K.; Stromstedt, P.E.; Rae, C.; Joenvall, H.; Flock, J.I.; Carlstedt-Duke, J. Biol. Chem. 264, 404-409, 1989  
 A;Title: High level expression in Escherichia coli of the DNA-binding domain of the g protein-coupled receptor gene  
 A;Reference number: A32196; MUID:89093147  
 A;Contents: annotation; domains  
 A;Note: engineered sequence expressed in Escherichia coli  
 R;Govindan, M.V.; Pothier, F.; Leclerc, S.; Palaniwami, R.; Xie, B.  
 J. Steroid Biochem. Mol. Biol. 40, 317-323, 1991  
 A;Title: Human glucocorticoid receptor gene promoter-homologous down regulation.  
 A;Reference number: 156596; MUID:92068829  
 A;Accession: 156596  
 A;Status: preliminary; translated from GB/EMBL/DDJB

A; Molecule type: DNA  
A; Residues: 1-394 <RES>  
A; Cross-references: GB:S68378; NID:9239757; PIDN:AAB20466\_1; PID:9239758  
C; Comment: Alpha and beta (see PIR:QRUGB) splice forms differ in their carboxyl-terminal  
C; Genetics:  
A; Gene: GDB:GRL  
A; Cross-references: GDB:120017; OMIM:138040  
A; Map position: 5q31-5q31  
A; Introns: 395/2; 451/1; 490/1; 583/1; 631/2; 675/1; 727/3  
A; Note: the first intron occurs before the initiator codon  
C; Superfamily: glucocorticoid receptor; erba transforming protein homology <ERBA>  
C; Keywords: alternative splicing; DNA binding; nucleus; steroid hormone receptor; trans-  
F; 421-441/Region: erba transforming protein homology <ERBA>  
F; 419-644/Region: zinc finger CCCC motif  
F; 728-777/Domain: steroid binding #status predicted <STB>

Query Match 19.4%; Score 856; DB 1; Length 777;  
Best Local Similarity 35.0%; Pred. No. 4e-37; Matches 239; Conservative 83; Mismatches 212; Indels 148; Gaps 25;  
Oy 248 SHSPAHASNVGSPLSPLSSMKSSISSPPSPHCSVKSPVSSPNNVTLSVSSPANINNR 307  
Db 6 SLTPGREENPSSYLAQERGVDMDFYKTLRGATTVKSASSPS----LAVASQSDSKR 60  
Oy 308 CSVSSPSNTNRRS---TLLSPAASTVG----SICSPVNNAATSYASG---TSAQSSPLR 356  
Db 61 LLYDVPKGKVSNAAQPDPLSKAVSULSMGLYMGMLYGETETKVMGNDLGFQPOQOISLSGETDLK 120  
Oy 357 DVVPS-----PDTQEKGQ-----EVFPFKTEEVESAISNGVGTGOLNIYVI 398  
Db 121 LLEESIANLNRSSTVSPVKSSASTAVSAAAPTKEFPEKTHSDVSEQDHLKGQ----- 173  
Oy 399 KPPDGAFGASSCGGNSN----NSDSSFSV-----PIKOESTKHSCTSGTSFKGNPT 446  
Db 174 -----TGTGNGNVKLYTIDQSTFDILQDEFFSSGSPKGKTNESPMRSDLIDENCL 224  
Oy 447 VNPFPPFMGDSYF-----SHMDDKYY----SLSGIGGPPVPGFDGNE 485  
Db 225 LSPLAGEDDSFLLEGNSNEDCKPLILPDPDKPKRDNGDLVLSSPSNVTLPOV----KTE 279  
Oy 486 GSF-----PVGKIQEPDGSYFPEASIPSSAVG-----VMSGGOSPHYRGA 529  
Db 280 KEDFIELCTPGVTKO-EKLGTVVQASCPGANIGKMSAISVHGVSsGGGOMVHYM----- 336  
Oy 530 QGTISLSRSARDQSFQHLLSSPPVNTLVESW----KSHGD-LSSRRSDGYPVLEYIPENV 584  
Db 337 -NTTASLSQQ-QDOK-PIFNVIPPIVGSENWNRCQSGDNLNLSLGTNFPGRTVFNSGY 393  
Oy 585 S5STLR-----SVSGSS-RPSKTCIYLVCGEASSCHYGVTGGSCKVFPRAVEGOH 635  
Db 394 SSPSMRPDVSSPSSSSSTATTGPPPKLCLVCSIDEASGHYGVLTGCGSKVFRKRAVEGOH 453  
Oy 636 NYLCAGRNDCIDKIRRNCPACRQLQKLOQAGNLGARKSKKGKLGIHEEQOPQQOPP 695  
Db 454 NYLCAGRNDCIDKIRRNCPACRQLQKLOQAGNLGARKSKKGKLGIHEEQOPQQOPP 695  
Oy 696 PPPPPPOSPEEGTYIAKAPERSVNTALVPOLSTISRALTPSPVMVLENIEPEPVYAGD 755  
Db 505 TGVSQETSENPGKTTIVPATLPQ-----LPTPTLVLSEVIEPPVLYAGD 549  
Oy 756 SSPPDTAISNLSTLNRLAGKOMIQVWKAWVLPGFKNUPLEDQITLQYSWMLSSFAIS 815  
Db 550 SSVPDSTWRIMTTLNMLGGRQVIAVKAWKATGPFRNLHDDQMTLQYSWMLMAFLG 609  
Oy 816 WRSYKHTNSQFLYFAPDLYFNE 837  
Db 610 WRSYROSSANLICFAPDLINE 631

glucocorticoid receptor - rat  
C; Species: Rattus norvegicus (Norway rat)  
C; Date: 31-Mar-1988 #sequence\_revision 31 Mar-1988 #text\_change 22-Jun-1999  
C; Accession: A24194  
R; Miesfeld, R.; Rusconi, S.; Godowski, P.J.; Maler, B.A.; Okret, S.; Wikstrom, A.C.;  
Cell 46, 389-399, 1986  
A; Title: Genetic complementation of a glucocorticoid receptor deficiency by expressio  
A; Reference number: A24194; MUID:86272086  
A; Molecular type: mRNA  
A; Residues: 1-795 <WIE>  
A; Cross-references: GB:MI4053; NID:9204271; PIDN:AAA1203\_1; PID:9204272  
R; Severne, Y.; Wieland, S.; Schaffner, W.; Rusconi, S.  
EMBO J. 7, 2303-2308, 1988  
A; Title: Metal binding 'finger' structures in the glucocorticoid receptor defined by  
A; Reference number: S02475; MUID:89052664  
A; Accession: S02475  
A; Status: not compared with conceptual translation  
A; Molecular type: mRNA  
A; Residues: 440-539 <SEV>  
R; Chang, C.; Kokontis, J.; Chang, C.T.; Liao, S.  
Nucleic Acids Res. 15, 9603, 1987  
A; Title: Cloning and sequence analysis of the rat ventral prostate glucocorti  
A; Reference number: A27284; MUID:88067783  
A; Accession: A27284  
A; Molecular type: mRNA  
A; Residues: 1-97, 'D', '99-225, 'G', '227-259, 'D', '261-344, 'T', '346-515 <CHA>  
A; Cross-references: GB:Y00480; NID:95324; PIDN:CAA68545\_1; PID:95325  
R; Gearling, K.L.; Gustafsson, J.A.; Okret, S.  
Nucleic Acids Res. 21, 1931-1933, 1993  
A; Title: Heterogeneity in the polyglutamine tract of the glucocorticoid receptor from  
A; Reference number: S33888; MUID:93261843  
A; Accession: S33888  
A; Status: preliminary  
A; Molecular type: DNA  
A; Residues: 68-97, 'D', '99-104 <GEA>  
A; Cross-references: EMBL:X69666  
A; Accession: S33891  
A; Status: preliminary  
A; Molecular type: DNA  
A; Residues: 68-92, '97, 'D', '99-104 <GE2>  
A; Cross-references: EMBL:X66669  
C; Comment: This sequence contains five potential translation initiators: 1-Met, 28-Me  
d is initiated from 1-Met.  
C; Superfamily: glucocorticoid receptor; erba transforming protein homology <ERBA>  
C; Keywords: DNA binding; nucleus; steroid hormone receptor; transcription regulation;  
F; 438-96/Region: glutamine-rich  
F; 440-460/Region: erba transforming protein homology <ERBA>  
F; 476-500/Region: zinc finger CCCC motif

Query Match 19.1%; Score 845.5; DB 1; Length 795;  
Best Local Similarity 30.1%; Pred. No. 1.4e-36; Matches 261; Conservative 88; Mismatches 235; Indels 283; Gaps 29;  
Oy 6 YHSUPEGLDMERRWGQVSQAVERSSLGPIPERTBNYMEIVNVCVSCAIPNNSTQGSSK 65  
Db 31 YKSLRGG-----ATVKVSSASSPSVAASQADSKQQTILLDS--KGSTSNVYQORQQQ 81  
Oy 66 EKQELLPCLQDNNRPGITLSDIKTELESKELSATVASEMGLY-----DSVRADYSSEQ 121  
Db 82 QQQQQQQQQQQQQQQPG-----LSKAVSLSMGLYMGETETKVMGNDLGFQ 127  
Oy 122 QNDQGMSMSPAKTIVONVEQVKFYKGNGHPRSTLSCVNTPRLSMSDGSVNGGVMRAIV 181  
Db 128 QGQIGLSSSETDFRLLEESI----- 147  
Oy 182 KSPIMCHERSPSVCSPLNTSSVCSPAGEINSVTSASFGSPVHSPTQGTLTCSPNA 241  
Db 148 -----ANLNRSSTSVE----NPKSSTSATGCACTPEKEPK-THSDSASEQ 188  
Oy 242 ENRGSRSHSPAHASNVGSPLSPLSSMKSSISSPPSPHCSVKSPVSSPNVTLSVSSPA 301  
RESULT 7  
QRRTG

Db 189 QNRKSR-----GTINGSVKLYPTQPOSTFDLK-DLEFSGSPKDNTNESPWRDILIDE 242  
 C;Keywords: alternative splicing; DNA binding; nucleus; steroid hormone receptor; tra  
 F;75-82/Region: glutamine-rich  
 F;426-680/Domain: erba transforming protein homology <ERBA>  
 F;426-448/Region: zinc finger CCCC motif  
 F;460-488/Region: zinc finger CCCC motif  
 F;734-783/Domain: steroid binding #status predicted <STB>

Db 302 NINNSRCVSSP----SNTNNRSTLSSPAASTVGSIICSPVNNAFSYTAGTSAGSSTLRD 357  
 C;Accession: S02214  
 A;Cross-references: EMBL:X13358; NID:951117; PID:CAM28031.1; PID:951058  
 A;Note: neither the complete nucleic acid sequence nor the complete translation are shown

Db 243 NLSPLAGEDDPFLLEGNTND-----CKP----- 267  
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 A;Molecule type: mRNA  
 A;Residues: 1-436; 'G', 438-458, 'R', 459-755 <NO2>  
 A;Cross-references: EMBL:X13359; NID:951119; PID:CAA31739.1; PID:951120  
 A;Note: neither the complete nucleic acid sequence nor the complete translation are shown

Db 418 NSDSSSV-IKQESTKHSCSGTFSKGNPNTVNPFFPMDSYFSFMDGAFFSSCLGGNSKI 417  
 C;Accession: S02214  
 A;Cross-references: EMBL:X13358; NID:951117; PID:CAM28031.1; PID:951058  
 A;Note: neither the complete nucleic acid sequence nor the complete translation are shown

Db 358 VVPSPMTQEKAQEVPPFKPEEVESAISNGVTGQLNIVQYIKPEPDGAFFSSCLGGNSKI 417  
 C;Accession: S02214  
 A;Cross-references: EMBL:X13359; NID:951119; PID:CAA31739.1; PID:951120  
 A;Note: neither the complete nucleic acid sequence nor the complete translation are shown

Db 268 -LTPDTK-----PKIQT----- 285  
 C;Accession: S02214  
 A;Cross-references: EMBL:X13358; NID:951117; PID:CAM28031.1; PID:951058  
 A;Note: neither the complete nucleic acid sequence nor the complete translation are shown

Db 428 NLSPLAGEDDPFLLEGNTND-----CKP----- 267  
 C;Accession: S02214  
 A;Cross-references: EMBL:X13358; NID:951117; PID:CAM28031.1; PID:951058  
 A;Note: neither the complete nucleic acid sequence nor the complete translation are shown

Db 477 VPGDGNCCEGSGFPVGKIQEQQDDGSYPEASIPSSAIVG-----VNSGQSFHY 525  
 C;Accession: S02214  
 A;Cross-references: EMBL:X13358; NID:951117; PID:CAM28031.1; PID:951058  
 A;Note: neither the complete nucleic acid sequence nor the complete translation are shown

Db 308 TPGV-----IKQE-KLGIVPCQASFGKNIIGNKMSAISVHGYSTSGCOMHY 354  
 C;Accession: S02214  
 A;Cross-references: EMBL:X13358; NID:951117; PID:CAM28031.1; PID:951058  
 A;Note: neither the complete nucleic acid sequence nor the complete translation are shown

Db 526 RIGAOCTISLRSARDOSFOHLSFRPVNTLVESENK-----SHDLS---SRR 570  
 C;Accession: S02214  
 A;Cross-references: EMBL:X13358; NID:951117; PID:CAM28031.1; PID:951058  
 A;Note: neither the complete nucleic acid sequence nor the complete translation are shown

Db 355 DM---NTASLSQ---QDOK-PVFWNVPPIPVGESENWNRCCOGSDEDSLTSLGALNFFGRSVF 409  
 C;Accession: S02214  
 A;Cross-references: EMBL:X13358; NID:951117; PID:CAM28031.1; PID:951058  
 A;Note: neither the complete nucleic acid sequence nor the complete translation are shown

Db 571 SDGYVPLEYLENSSSTLRLYSTGSSRSPSKICLVCGLGDEASGCHYGWTGSCKVFEKRA 630  
 C;Accession: S02214  
 A;Cross-references: EMBL:X13358; NID:951117; PID:CAM28031.1; PID:951058  
 A;Note: neither the complete nucleic acid sequence nor the complete translation are shown

Db 410 SNGYSSPGMRPDVSSPSSAAATGP---PPKLCIYLVSDEASGCHYGVLTGSCKVFEKRA 467  
 C;Accession: S02214  
 A;Cross-references: EMBL:X13358; NID:951117; PID:CAM28031.1; PID:951058  
 A;Note: neither the complete nucleic acid sequence nor the complete translation are shown

Db 631 VEGQHNYLCAGRNDCTDKIRRNKCAPCRLQCLQAGMNLGARKSKKLKGKUHGHEEQPO 690  
 C;Accession: S02214  
 A;Cross-references: EMBL:X13358; NID:951117; PID:CAM28031.1; PID:951058  
 A;Note: neither the complete nucleic acid sequence nor the complete translation are shown

Db 468 VEGQHNYLCAGRNDCTDKIRRNKCAPCRLQCLQAGMNLGARKSKKLKGKUHGHEEQPO 525  
 C;Accession: S02214  
 A;Cross-references: EMBL:X13358; NID:951117; PID:CAM28031.1; PID:951058  
 A;Note: neither the complete nucleic acid sequence nor the complete translation are shown

Db 691 QQQPPPPPPPOSEPECTTYIAPAKEPSVNTALVPLSTISRALTPSPVVMLENTEPEIV 750  
 C;Accession: S02214  
 A;Cross-references: EMBL:X13358; NID:951117; PID:CAM28031.1; PID:951058  
 A;Note: neither the complete nucleic acid sequence nor the complete translation are shown

Db 526 VSQ-----DTSENPKTVPAALPQ-----LTPTLVSLLEPEPEVL 562  
 C;Accession: S02214  
 A;Cross-references: EMBL:X13358; NID:951117; PID:CAM28031.1; PID:951058  
 A;Note: neither the complete nucleic acid sequence nor the complete translation are shown

Db 751 YAGYDSSSKPDTAENLILSTLNRLAGKOMIQVVKWAKVLPGFKNLPLEDQITLIQYSMCLS 810  
 C;Accession: S02214  
 A;Cross-references: EMBL:X13358; NID:951117; PID:CAM28031.1; PID:951058  
 A;Note: neither the complete nucleic acid sequence nor the complete translation are shown

Db 563 YAGYDSSVPDASKRIMTINLMGROVIAAVKWAIAKALGLRNLHDDQMLULQYSMFLM 622  
 C;Accession: S02214  
 A;Cross-references: EMBL:X13358; NID:951117; PID:CAM28031.1; PID:951058  
 A;Note: neither the complete nucleic acid sequence nor the complete translation are shown

Db 811 SPALSWYKHNISOFTYFADLVFNE 837  
 C;Accession: S02214  
 A;Cross-references: EMBL:X13358; NID:951117; PID:CAM28031.1; PID:951058  
 A;Note: neither the complete nucleic acid sequence nor the complete translation are shown

Db 623 ARALGWWSYROSQSGNLICFAPOLINE 649  
 C;Accession: S02214  
 A;Cross-references: EMBL:X13358; NID:951117; PID:CAM28031.1; PID:951058  
 A;Note: neither the complete nucleic acid sequence nor the complete translation are shown

RESULT 8  
 Db 25691 glucocorticoid receptor - mouse  
 C;Species: Mus musculus (house mouse)  
 C;Accession: A25691; S02214  
 R;Danielsen, M.; Northrop, J.P.; Ringold, G.M.  
 EMB J. 5, 2513-2522, 1986  
 A;Title: The mouse glucocorticoid receptor: mapping of functional domains by cloning, sequencing and mutagenesis  
 A;Reference number: A25691; MUID:87053816  
 A;Accession: A25691  
 A;Molecule type: mRNA  
 A;Residues: 1-783 <DAN>  
 A;Cross-references: GB:X04435; NID:951057; PID:CAM28031.1; PID:951058  
 R;Nozono, T.; Kasai, Y.; Saito, T.  
 Nucleic Acids Res. 17, 445, 1989  
 A;Title: Novel cDNA sequence possibly generated by alternative splicing of a mouse glucocorticoid receptor  
 A;Reference number: S02212; MUID:89098404  
 A;Accession: S02212  
 A;Molecule type: mRNA  
 A;Residues: 1-436, 'G', 438-458, 'R', 459-755 <NO2>  
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 A;Note: neither the complete nucleic acid sequence nor the complete translation are shown

Db 286 SSPSSVALPOVTEK----- 307  
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 A;Cross-references: EMBL:X13358; NID:951117; PID:CAM28031.1; PID:951058  
 A;Note: neither the complete nucleic acid sequence nor the complete translation are shown

Db 358 VVPSPMTQEKAQEVPPFKPEEVESAISNGVTGQLNIVQYIKPEPDGAFFSSCLGGNSKI 417  
 C;Accession: S02214  
 A;Cross-references: EMBL:X13359; NID:951119; PID:CAA31739.1; PID:951120  
 A;Note: neither the complete nucleic acid sequence nor the complete translation are shown

Db 268 -LTPDTK-----PKIQT----- 285  
 C;Accession: S02214  
 A;Cross-references: EMBL:X13358; NID:951117; PID:CAM28031.1; PID:951058  
 A;Note: neither the complete nucleic acid sequence nor the complete translation are shown

Db 428 NLSPLAGEDDPFLLEGNTND-----CKP----- 267  
 C;Accession: S02214  
 A;Cross-references: EMBL:X13358; NID:951117; PID:CAM28031.1; PID:951058  
 A;Note: neither the complete nucleic acid sequence nor the complete translation are shown

Db 477 VPGDGNCCEGSGFPVGKIQEQQDDGSYPEASIPSSAIVG-----VNSGQSFHY 525  
 C;Accession: S02214  
 A;Cross-references: EMBL:X13358; NID:951117; PID:CAM28031.1; PID:951058  
 A;Note: neither the complete nucleic acid sequence nor the complete translation are shown

Db 308 TPGV-----IKQE-KLGIVPCQASFGKNIIGNKMSAISVHGYSTSGCOMHY 354  
 C;Accession: S02214  
 A;Cross-references: EMBL:X13358; NID:951117; PID:CAM28031.1; PID:951058  
 A;Note: neither the complete nucleic acid sequence nor the complete translation are shown

Db 526 RIGAOCTISLRSARDOSFOHLSFRPVNTLVESENK-----SHDLS---SRR 570  
 C;Accession: S02214  
 A;Cross-references: EMBL:X13358; NID:951117; PID:CAM28031.1; PID:951058  
 A;Note: neither the complete nucleic acid sequence nor the complete translation are shown

Db 355 DM---NTASLSQ---QDOK-PVFWNVPPIPVGESENWNRCCOGSDEDSLTSLGALNFFGRSVF 409  
 C;Accession: S02214  
 A;Cross-references: EMBL:X13358; NID:951117; PID:CAM28031.1; PID:951058  
 A;Note: neither the complete nucleic acid sequence nor the complete translation are shown

Db 571 SDGYVPLEYLENSSSTLRLYSTGSSRSPSKICLVCGLGDEASGCHYGWTGSCKVFEKRA 630  
 C;Accession: S02214  
 A;Cross-references: EMBL:X13358; NID:951117; PID:CAM28031.1; PID:951058  
 A;Note: neither the complete nucleic acid sequence nor the complete translation are shown

Db 410 SNGYSSPGMRPDVSSPSSAAATGP---PPKLCIYLVSDEASGCHYGVLTGSCKVFEKRA 467  
 C;Accession: S02214  
 A;Cross-references: EMBL:X13358; NID:951117; PID:CAM28031.1; PID:951058  
 A;Note: neither the complete nucleic acid sequence nor the complete translation are shown

Db 631 VEGQHNYLCAGRNDCTDKIRRNKCAPCRLQCLQAGMNLGARKSKKLKGKUHGHEEQPO 690  
 C;Accession: S02214  
 A;Cross-references: EMBL:X13358; NID:951117; PID:CAM28031.1; PID:951058  
 A;Note: neither the complete nucleic acid sequence nor the complete translation are shown

Db 468 VEGQHNYLCAGRNDCTDKIRRNKCAPCRLQCLQAGMNLGARKSKKLKGKUHGHEEQPO 525  
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 A;Note: neither the complete nucleic acid sequence nor the complete translation are shown

Db 691 QQQPPPPPPPOSEPECTTYIAPAKEPSVNTALVPLSTISRALTPSPVVMLENTEPEIV 750  
 C;Accession: S02214  
 A;Cross-references: EMBL:X13358; NID:951117; PID:CAM28031.1; PID:951058  
 A;Note: neither the complete nucleic acid sequence nor the complete translation are shown

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 A;Cross-references: EMBL:X13358; NID:951117; PID:CAM28031.1; PID:951058  
 A;Note: neither the complete nucleic acid sequence nor the complete translation are shown

Db 751 YAGYDSSSKPDTAENLILSTLNRLAGKOMIQVVKWAKVLPGFKNLPLEDQITLIQYSMCLS 810  
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 A;Cross-references: EMBL:X13358; NID:951117; PID:CAM28031.1; PID:951058  
 A;Note: neither the complete nucleic acid sequence nor the complete translation are shown

Db 563 YAGYDSSVPDASKRIMTINLMGROVIAAVKWAIAKALGLRNLHDDQMLULQYSMFLM 622  
 C;Accession: S02214  
 A;Cross-references: EMBL:X13358; NID:951117; PID:CAM28031.1; PID:951058  
 A;Note: neither the complete nucleic acid sequence nor the complete translation are shown

Db 811 SPALSWYKHNISOFTYFADLVFNE 837  
 C;Accession: S02214  
 A;Cross-references: EMBL:X13358; NID:951117; PID:CAM28031.1; PID:951058  
 A;Note: neither the complete nucleic acid sequence nor the complete translation are shown

Db 623 ARALGWWSYROSQSGNLICFAPOLINE 649  
 C;Accession: S02214  
 A;Cross-references: EMBL:X13358; NID:951117; PID:CAM28031.1; PID:951058  
 A;Note: neither the complete nucleic acid sequence nor the complete translation are shown

Query Match 19 0%; Score 842; DB 1; Length 783;  
 Best Local Similarity 30.6%; Pred. No. 2.1e-36;  
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 F;426-680/Domain: erba transforming protein homology <ERBA>  
 F;426-448/Region: zinc finger CCCC motif  
 F;460-488/Region: zinc finger CCCC motif  
 F;734-783/Domain: steroid binding #status predicted <STB>

Db 477 VPGDGNCCEGSGFPVGKIQEQQDDGSYPEASIPSSAIVG-----VNSGQSFHY 525  
 C;Accession: S02214  
 A;Cross-references: EMBL:X13358; NID:951117; PID:CAM28031.1; PID:951058  
 A;Note: neither the complete nucleic acid sequence nor the complete translation are shown

Db 308 TPGV-----IKQE-KLGIVPCQASFGKNIIGNKMSAISVHGYSTSGCOMHY 354  
 C;Accession: S02214  
 A;Cross-references: EMBL:X13358; NID:951117; PID:CAM28031.1; PID:951058  
 A;Note: neither the complete nucleic acid sequence nor the complete translation are shown

Db 526 RIGAOCTISLRSARDOSFOHLSFRPVNTLVESENK-----SHDLS---SRR 570  
 C;Accession: S02214  
 A;Cross-references: EMBL:X13358; NID:951117; PID:CAM28031.1; PID:951058  
 A;Note: neither the complete nucleic acid sequence nor the complete translation are shown

Db 355 DM---NTASLSQ---QDOK-PVFWNVPPIPVGESENWNRCCOGSDEDSLTSLGALNFFGRSVF 409  
 C;Accession: S02214  
 A;Cross-references: EMBL:X13358; NID:951117; PID:CAM28031.1; PID:951058  
 A;Note: neither the complete nucleic acid sequence nor the complete translation are shown

Db 571 SDGYVPLEYLENSSSTLRLYSTGSSRSPSKICLVCGLGDEASGCHYGWTGSCKVFEKRA 630  
 C;Accession: S02214  
 A;Cross-references: EMBL:X13358; NID:951117; PID:CAM28031.1; PID:951058  
 A;Note: neither the complete nucleic acid sequence nor the complete translation are shown

Db 410 SNGYSSPGMRPDVSSPSSAAATGP---PPKLCIYLVSDEASGCHYGVLTGSCKVFEKRA 467  
 C;Accession: S02214  
 A;Cross-references: EMBL:X13358; NID:951117; PID:CAM28031.1; PID:951058  
 A;Note: neither the complete nucleic acid sequence nor the complete translation are shown

Db 631 VEGQHNYLCAGRNDCTDKIRRNKCAPCRLQCLQAGMNLGARKSKKLKGKUHGHEEQPO 690  
 C;Accession: S02214  
 A;Cross-references: EMBL:X13358; NID:951117; PID:CAM28031.1; PID:951058  
 A;Note: neither the complete nucleic acid sequence nor the complete translation are shown

Db 468 VEGQHNYLCAGRNDCTDKIRRNKCAPCRLQCLQAGMNLGARKSKKLKGKUHGHEEQPO 525  
 C;Accession: S02214  
 A;Cross-references: EMBL:X13358; NID:951117; PID:CAM28031.1; PID:951058  
 A;Note: neither the complete nucleic acid sequence nor the complete translation are shown

Db 691 QQQPPPPPPPOSEPECTTYIAPAKEPSVNTALVPLSTISRALTPSPVVMLENTEPEIV 750  
 C;Accession: S02214  
 A;Cross-references: EMBL:X13358; NID:951117; PID:CAM28031.1; PID:951058  
 A;Note: neither the complete nucleic acid sequence nor the complete translation are shown

Db 526 VSQ-----DTSENPKTVPAALPQ-----LTPTLVSLLEPEPEVL 562  
 C;Accession: S02214  
 A;Cross-references: EMBL:X13358; NID:951117; PID:CAM28031.1; PID:951058  
 A;Note: neither the complete nucleic acid sequence nor the complete translation are shown

Db 751 YAGYDSSSKPDTAENLILSTLNRLAGKOMIQVVKWAKVLPGFKNLPLEDQITLIQYSMCLS 810  
 C;Accession: S02214  
 A;Cross-references: EMBL:X13358; NID:951117; PID:CAM28031.1; PID:951058  
 A;Note: neither the complete nucleic acid sequence nor the complete translation are shown

Db 563 YAGYDSSVPDASKRIMTINLMGROVIAAVKWAIAKALGLRNLHDDQMLULQYSMFLM 622  
 C;Accession: S02214  
 A;Cross-references: EMBL:X13358; NID:951117; PID:CAM28031.1; PID:951058  
 A;Note: neither the complete nucleic acid sequence nor the complete translation are shown

Db 811 SPALSWYKHNISOFTYFADLVFNE 837  
 C;Accession: S02214  
 A;Cross-references: EMBL:X13358; NID:951117; PID:CAM28031.1; PID:951058  
 A;Note: neither the complete nucleic acid sequence nor the complete translation are shown

Db 623 ARALGWWSYROSQSGNLICFAPOLINE 649  
 C;Accession: S02214  
 A;Cross-references: EMBL:X13358; NID:951117; PID:CAM28031.1; PID:951058  
 A;Note: neither the complete nucleic acid sequence nor the complete translation are shown

RESULT 9  
 153280 progesterone receptor B form - rat  
 C;Species: Rattus norvegicus (Norway rat)  
 C;Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 20-Aug-1999  
 C;Accession: I53280; B23733; A49574; A23733  
 R;Park-Sarge, O.K.; Mayo, K.E.  
 Endocrinology 134, 709-718, 1994  
 A;Title: Regulation of the progesterone receptor gene by gonadotropins and cyclic adenosine monophosphate  
 A;Reference number: I53280; MUID: 94130817  
 A;Accession: I53280  
 A;Status: preliminary; translated from GB/EMBL/DBDJ  
 A;Molecule type: mRNA  
 A;Residues: 1-923 <PAR1>  
 A;Cross-references: GB:L16922; NID:9463282; PIDN:AAA19916.1; PID:9463283  
 R;Park, O.K.; Mayo, K.E.  
 Mol. Endocrinol. 5, 967-978, 1991  
 A;Title: Transient expression of progesterone receptor messenger RNA in ovarian granulosa cells  
 A;Reference number: A23733; MUID: 92049379  
 A;Accession: B23733  
 A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual translation  
 A;Molecule type: mRNA  
 A;Residues: 555-589; 'W' 591-624; 742-910 <PAR2>  
 A;Cross-references: GB:S64044  
 Mol. Endocrinol. 7, 1603-1616, 1993  
 A;Title: Cloning of the rat progesterone receptor gene 5'-region and identification of t  
 A;Reference number: A49574; MUID: 94195318  
 A;Accession: A49574  
 A;Status: preliminary; translated from GB/EMBL/DBDJ  
 A;Molecule type: DNA  
 A;Residues: 1-16 <KRA>  
 A;Cross-references: GB:S69361; NID:9546178  
 C;Superfamily: Progesterone receptor; erbA transforming protein homology  
 C;Keywords: DNA binding; nucleus; steroid hormone receptor; zinc finger  
 F;557-577/Region: erbA transforming protein homology <ERBA>  
 F;593-617/Region: zinc finger

Query Match 18.6%; Score 823.; DB 2; Length 923;  
 Best Local Similarity 31.7%; Pred. No. 2, 6e-35;  
 Matches 260; Conservative 95; Mismatches 226; Indels 238; Gaps 37;

QY 216 TTASCGSFPVHSPIRQTPILCSPNAENRQRSHPAHASNVGSPPLSSPMKSISSP 275  
 Db 11 TLHTSGAAP--SPTHVGSPILLARLUPDPFEGSOHS--DASSVVPISUDRLPSR-- 64

QY 276 PSHCSVKS-PVSSPNNVTLRSSV-----SSPANINNSRC-----SVSSP 313  
 Db 65 --CQAELEDEKTQNQQLSDVECAFSGVERAARRSRNRAPEDRSRLDSVLTLAP 121

QY 314 SNTNNRSTLSSPAASIVGSC-----SPVNV--AFSYTASGTSA 350  
 Db 122 SGPEOSQT-SPPACEAITSWCLFGPELPEDPRSVPATKGELSPMSRPESKAQDGGTGA 180

QY 351 GSSTLRDVWSPDPO-----EKAQAEVFPKTEVEAISNGTQOLNIVQYI 398  
 Db 181 GOKVLPKAV-SPPRQLLPLPTSGSAIHWPAGVVKPSQOOPATVEEE--DGGLETEGSAGPLL 237

QY 399 KPEPDGAFSSCLGGNSKINS-----DSSFSVP---IKQES----- 431  
 Db 238 KSKP-RALEGNCSSGGVTANAPGGAPGGVTLVPKEDSRSFAPRSLEQADPVAAPRSPLA 296

QY 432 -----TKHCSGTSFKGNPTVNPFFMDGSYFSFMDDKDYYS 468

Db 297 TTVVPIHWPLPHALLARTROLLEGESYDGGAAQVFPAPPGRS 344

QY 469 LSGIIGPPPVGFDF-----GNGCEGSGGPV-----GIK-QPDDGSY----- 502

Db 345 -PSAFSPPPVFCGDFPDCTYPPEGDFPDKEDGFVPGFVYGEROPPGLIKKEBEGEAEARSRRPY 403

QY 503 -----YP-----EASTI-PSSAIVGVNNSGQSFH--YRI-GA- 529

---

RESULT 10  
 S60586  
 glucocorticoid receptor - rainbow trout  
 C;Species: Oncorhynchus mykiss (rainbow trout)  
 C;Date: 27-Apr-1996 #sequence\_revision 13-Mar-1997 #text\_change 20-Aug-1999  
 C;Accession: S60586; S70470  
 R;Ducourte, B.; Tujague, M.; Ashraf, J.; Mouchel, N.; Servel, N.; Valotaire, Y.; Thom Endocrinology 116, 3737-3741, 1995  
 A;Title: Cloning of a teleost, fish glucocorticoid receptor shows that it contains a d  
 A;Reference number: S60586; MUID: 95377204  
 A;Accession: S60586  
 A;Molecule type: mRNA  
 A;Residues: 1-738 <DUC>  
 A;Cross-references: EMBL:254210; NID:995676; PIDN:CAA9937.1; PID:995677  
 R;Takeo, J.; Hata, J.; Seawa, C.; Toyohara, H.; Yamashita, S.  
 FEBS Lett. 389, 244-248, 1996  
 A;Title: Fish glucocorticoid receptor with splicing variants in the DNA binding domain  
 A;Reference number: S70470; MUID: 96335602  
 A;Accession: S70470  
 A;Molecule type: mRNA  
 A;Residues: 1-89 'L', 91-246, 'P', 248-281, 'Y', 283-303, 'T', 305-351, 'RLI', 355, 'S', 357-444  
 A;Experimental source: pituitary  
 A;Gene: GR  
 A;Genetics:  
 C;Superfamily: glucocorticoid receptor; erbA transforming protein homology  
 C;Keywords: alternative splicing; DNA binding; steroid binding; transcription regulation  
 F;59-69/Region: glutamine-rich  
 F;385-469/Region: erbA transforming protein homology <ERBA>  
 F;37-40/Region: zinc finger CCCC motif  
 F;432-456/Region: zinc finger CCCC motif  
 F;703-752/Region: steroid binding #status predicted <STB>

Query Match 18.4%; Score 814.5; DB 2; Length 758;  
 Best Local Similarity 33.8%; Pred. No. 5 5e-35;  
 Matches 229; Conservative 79; Mismatches 228; Indels 141; Gaps 21;

QY 212 SVSSTASFGFPPVHPITDGPICLTCSPNAENRQRSHPHASNVGSPPLSSP----- 264  
 Db 20 SESSVGSFSGDTGGSKSTSTSMLHP---GSRPQPADSANGLNVTQMLSTG 74

QY 265 -LSSMSSISSSPSPHSCHSVKSPVSSPNNVTLRSSV--SSPANINNSRCVVSPSNTNNR 319  
 Db 75 GLTIEAAVKMEKARMQDQPKPQONQQLFENALLESTADNR-----SNPGS 126



Db	484	AKWLGGRKKFLINKKVKVRIIDVALQQPAVIQDETOISLQLSF- SPNQE-----IP	535
Qy	726	OLSTISRALKTSPVWLENTEPEIIVYAGDSKPDATTAENLLSTINRLAGKOMIQVVKWA	785
Db	536	-----FVPPMISVLRGIEPEVVYAGDVKHPTPSSSLTSLNHICERQLCCKVWK	587
Qy	786	VLPGFKNLPLEQDITLQYQSMCLSSPMSWYSKPHNSQFLYFAPDLVFNELLARVE	844
Db	588	LLPGFRNLHIDQDITLIQYQSMMSLMLVFGAMWRSYKHVGQMLYFAPDLLINE--ORMKE	644
RESULT	12		
A39596		progesterone receptor B form - mouse	
C;Species:	Mus musculus (house mouse)		
C;Date:	20-Mar-1992 #sequence_revision	20-Mar-1992 #text_change	20-Aug-1999
R;Schott, D.R.; Shyamala, G.; Schneider, W.; Parry, G.			
Biochemistry 30, 7047-7020, 1991			
A;Title: Molecular cloning, sequence analyses, and expression of complementary DNA encoded by the ERB-B2 gene.			
A;Reference number: A39596; MUID: 91299759			
A;Status: preliminary			
A;Molecule type: mRNA			
A;Residues: 1-933 <SCH>			
A;Cross-references: GB: M68915; GB: J05333; NID: q200471; PIDN: AAA39971.1; PID: g200472			
R;Hagiwara, K.; Wu-Peng, X.S.; Funabashi, T.; Kato, J.; Pfaff, D.W.			
Biochem. Biophys. Res. Commun. 205, 1093-1101, 1994			
A;Title: Nucleic acid sequence and DNA hypersensitive sites of the 5' region of the md			
A;Reference number: 149111; MUID: 95100931			
A;Accession: I49111			
A;Status: preliminary; translated from GB/EMBL/DDJB			
A;Molecule type: DNA			
A;Residues: 1-9 <HAG>			
A;Cross-references: EMBL: U12644; NID: g639916; PIDN: AAA66067.1; PID: g639917			
C;Superfamily: progesterone receptor; erbA transforming protein homology			
C;Keywords: DNA binding; nucleus; steroid hormone receptor; transcription regulation; zinc finger			
Oy		Query Match	
Best Local Similarity	18.2%	Score	804; DB
Matches	30,33;	Pred.	No. 2_5e-34;
251;	Conservative		
94;	Mismatches		
249;	Indels		
234;	Gaps		
Oy		Length	923;
181	VKSPIMCH-EKSPVCSPPLMTSSVCSPEGIN-----SVSS	215	
Db	24	IGSPULLARLDSGPFGFOGSOHSVSSVSPPISTDGLGFLPRSCRGPELPDKKGQDQQLSD	83
Qy	216	TTASFGSFPVHSPITOQGTPCTSPNAENRGRSRSHSAHAHN--VGSPLSPL--SSMKSS	271
Db	84	VEGAF-----SGVEAT----HREGGRNRPEKDSRLLSDVLDLSLTPSGEQS	128
Qy	272	ISSSPHCSCVS-----EVSSPNNVTRSSVSVSPANINNSRCVSSPSNTNRSTLS	323
Db	129	HASPACATEITSWCLFGPELP-EDPRSVPATKGLLSP-LMSRPEIKVGQSGTGRGOKVL	186
Qy	324	SPAASVGSICSPVNNAFSTVAGTSAGSSTLRDVPSDQEKGAOEVPPKTEEVESA	383
Db	187	PKGLSPRQLLPTSGSAHNPAGG-----VRKSPQ-----PAAGEEE-	224
Qy	384	ISNGVGTQQLNIVQYIKPEPDAFQFSSCLGIGNSKNS-----DSSFSVP--	426
Db	225	-DSGLETEGASPLKLSSKPRALEGTCQGGVAANAPSAPOGVTLVKEDSRFSAPRS	282
Oy	427	IROES-----TKHCSGTSFPKGPNIVNP-----	450
Db	283	LEQDSTPATGRSPLATWVDFTHVPLPLNHALAARTROLLEGESDGATAGPFCPPR	342
Oy	451	--PFMDCSYFSEMDDK-DYIYSLG-----ILGPVPVG	479
RESULT	13		
QRRUP		progesterone receptor form B - human	
N;Alternate names:	hPR		
N;Contains:	Progesterone receptor form A		
C;Species:	Homo sapiens (man)		
C;Date:	30-Jun-1987 #sequence_revision	18-Nov-1994 #text_change	22-Jun-1999
C;Accession:	S09971; S2464; A03245		
R;Kastner, P.; Krust, A.; Turcotte, B.; Stropp, U.; Tora, L.; Gronemeyer, H.; Chambon			
EMBO J. 9, 1603-1614, 1990			
A;Title: Two distinct estrogen-regulated promoters generate transcripts encoding the			
A;Reference number: S09971; MUID: 9022361			
A;Accession: S09971			
A;Molecule type: mRNA			
A;Residues: 1-933 <KAS>			
A;Cross-references:	EMBL: X51730		
R;Kastner, P.			
submitted to the EMBL Data Library, February 1990			
A;Reference number:	S12464		
A;Accession:	S12464		
A;Molecule type: mRNA			
A;Residues:	1-343, 'T', 345-933 <KA2>		
A;Cross-references:	EMBL: X51730; NID: g35651; PIDN: CA36018.1; PID: g35652		
R;Misrahi, M.; Attie, M.; D'Auriol, L.; Loosfelt, H.; Meriel, C.; Fridlansky, F.; Giul			
Biochem. Biophys. Res. Commun. 143, 740-748, 1987			
A;Title: Complete amino acid sequence of the human progesterone receptor deduced from the cDNA sequence.			
A;Accession:	A03245		
A;Molecule type: mRNA			
A;Residues:	1-225, 'G', 227-255, 'V', 257-659, 'V', 661-933 <MS>		
A;Cross-references:	GB: M15716; NID: g189934; PIDN: AAA60081.1; PID: g189935		
C;Genetics:			
A;Gene:	GDB: PGR		
A;Cross-references:	GDB: 119493; OMIM: 264080		
A;Map position:	11q22.1-11q22.3		
C;Superfamily:	Progesterone receptor; erbA transforming protein homology		
C;Keywords:	alternative splicing; DNA binding; nucleus; phosphoprotein; steroid hormone		
F;1-933/Product:	Progesterone receptor form B #status predicted <MA1>		
F;165-933/Product:	Progesterone receptor form B #status predicted <MA2>		
F;565-839/Domain:	erbA transforming protein homology <ERBA>		
F;567-587/Region:	zinc finger CCCC motif		
F;603-627/Region:	zinc finger CCCC motif		

F;681-933/domain: steroid binding #status predicted <SPB>  
 F;41/Binding site: phosphate (Thr) (covalent) #status predicted  
 F;227,232,552,793/Binding site: phosphate (Ser) (covalent) #status predicted  
 F;329,374,601/Binding site: phosphate (Tyr)(covalent) #status predicted

Progesterone receptor - rabbit  
 C:Species: Oryctolagus cuniculus (domestic rabbit)  
 C:Date: 16-Aug-1988 #sequence\_revision 16-Aug-1988  
 C:Accession: A25923  
 R:Loosfelt, H.; Atger, M.; Misrahi, M.; Guiuchon-Mantel, A.; Meriel, C.; Logeat, F.;

Proc. Natl. Acad. Sci. U.S.A. 83, 9045-9049, 1986

A:Title: Cloning and sequence analysis of rabbit progesterone-receptor complementary

A:Reference number: A25923

A:Molecule type: mRNA

A:Cross-references: GB:MI4547; NID:gi16531; PIDN:AAA31443.1; PID:g16563.2

C:Superfamily: Progesterone receptor; erba transforming protein homology <ERBA>

C:Keywords: DNA binding; nucleus; steroid hormone receptor; transcription regulation;

F;568-826/domain: erba transforming protein homology <ERBA>

F;568-588/Region: zinc finger

F;604-628/Region: zinc finger

Query	Match	Score	DB	Length
QY	191 SPSVCSPUNMNTSSVCSAG---INSVSSTAASFGRPVHSRPIOTG--PLTC--SPNA	241	1	933;
Db	20 SPEVGSPL----LCRPAAGPFPGSQTSDTPEVSAIPIS--LDGLFPFRPCQ3QPDSD	71		
QY	242 EN-----RGSRSHSPANASNVGSPLSPP-----LSMKSISLSSPNSHCYSKSPV	285		
Db	72 EKTDQDQSLSDVEGAYSSRAEATRGAGGSSSSPPEKDQGLDPSVLTLAP-----	121		
QY	286 SSPNNVTLRSSVSSPANTNNRCSVSS-----PSNTNNRSTLSSPAASTVGSCSP	336		
Db	122 SGPG---QSQFSFP-----CEVTSWCLQGPPELPED-----PPAPATORTLSP	163		
QY	337 VNPRAFSYTASGTSAGSSTSRLDVVP----SPDTQ-----EKGAQEVPF-----KTE	378		
Db	164 LMSR-SGCKVGDSSGTAAHKVLRFLRGLSPARQLLIPASESPHWSGAVVKPSLQAAVE	222		
QY	379 EVSSAISNGVTGDLINIVYIKPEP-----DGAFSSC-----LGGSNSKI-NSDSSFSV	425		
Db	223 EDSSESEESBAGPL----LKGKPRALGGAAGGAAACPPGAAGGVALVEKFEDRSFA	277		
QY	426 P---IKOES-----TKHSCSGTSFKG-----443			
QY	466 -----YYSIGI-----LGPPVP-----GFD	481		
Db	278 PRVILVEQDAPMAGRSPLATTYNDIHVPLPILNHALLAARTRQLLEDESTDGGAGAAS	337		
QY	444 -----NPTVNPFP-----FMDCSYFSFMDDK-----465			
Db	338 AFAPPRSSFCASSTPVAVGDFPDCAVPPDAEPKDAYPIYSDQFOPPAIKIKEEEGAEAS	397		
QY	466 -----YYSIGI-----LGPPVP-----GFD	481		
Db	398 ARSPRSYLVAGANAAFPDPDPLGPPLPPRATESRPGEAAVTAPASAVERSASSGST	457		
QY	482 GNC-----EGSGPPGIGIQEPDGSYVEASIPSSATVGUNSGGOSFY-RIGA	529		
QY	458 LECTILYKAEGAPPOGPFAAPPCKAPAGSCLIPRDGLPSTSASAAAAGAAPALYPALGL	517		
Db	530 QGTISLISRSARDQSFQHLLSSPPPTNLVESWKSIGDLSSRRSDCQPYLEI-FENVSST	588		
QY	518 NGLPQLGYQAVLK---BGLPQVY-----PYLNLYRIPSEASOS	554		
Db	589 LRSVSTGSSRPSKTCILVCGDEASGCHYGVMTGCKVKFRAVQHNLICAGRNDCCID	648		
QY	555 PQ-YSFESLFOKICLICGDEASCHYGVLTGCKVFKEGRAMQHNLICAGRNDCTVD	612		
QY	649 KIRRNCPACRLQKLOQAGNIGAKSKKKGKKGKIGHE-EQPOQQQOPPPPPPOSPEG	707		
Db	613 KIRRNCPACRLRKCGQAGVIGRKRFKENKVRVRAVALAVLQPLGVPNEQALSQR	672		
Db	708 TTYIAPAKESVNTALVPLQSTISRALTSPPMVMENTIEPIVIVAGYDASKPDAAENLIS	767		
QY	673 FTF-----SPGQDQIQLPPL-----INLLMSIEDPVTVAGHDNTPDQISSLIT	716		
Db	768 TLNRLAGKQMTQVWKWAKVLPFGKNUPLQDQITLIQYSWMCILSFAFSWRSYKINTSQEL	827		
QY	717 SLNQLGERQQLSVWVKNSLPGFRNHLDDQITLIQYSWMSLMLVGLGWRSYKIVSGML	776		
QY	828 YFAPDVLVNEELLARVRE	844		
Db	777 YFAPDVLLINE-ORMKE	791		

RESULT 14

A25923

Db 685 -----INLIMSTEPDVYAGHDNTKPDTSLLSLNQLEROLLSVWKWSKSLP 734  
 Qy 789 GRKKNLPLEDQTILIQSWMCISSEALSWRSYKHTNSQFLYFADPLVNELLARVRE 844  
 Db 735 GFRNLHIDQDITLIQYSWMSLMVFGLWRSTKHVGOMLYFRPDLINE-QRMKE 788  
 F:650-899/Domain: hormone binding #status predicted <LIG>

C:Keywords: DNA binding; transcription regulation; zinc finger  
 F:1-55/Domain: regulatory #status predicted <REG>  
 F:537-95/Domain: erba transforming protein homology <ERBA>  
 A:Title: Molecular cloning of androgen receptors from divergent species with a polymerase cDNA probes from dog, guinea pig and clawed frog.  
 A:Reference number: A35895; MUID:90386642  
 A:Accession: A35895  
 A:Molecule type: mRNA  
 A:Residues: 1-899 <HEX>  
 A:Cross-references: EMBL:X53779; NID:949966; PIDN:CAA37795.1; PID:949967  
 Mol: Endocrinol. 4, 1600-1610, 1990  
 R: Gaspar, M.L.; Meo, T.; Tosi, M.  
 A:Title: Structure and size distribution of the androgen receptor mRNA in wild-type and  
 A:Reference number: A37255; MUID:91133433  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-899 <GAS>  
 A:Cross-references: GB:M37890; NID:9191935; PIDN:AAA37234.1; PID:9191936  
 R:Charest, N.J.; Zhou, Z.; Lubahn, D.B.; Olsen, K.L.; Wilson, E.M.; French, F.S.  
 Mol: Endocrinol. 5, 573-581, 1991  
 A:Title: A frameshift mutation destabilizes androgen receptor messenger RNA in the Tfm rat  
 A:Reference number: A37908; MUID:92017874  
 A:Accession: A37908  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-899 <CHA>  
 A:Cross-references: GB:S56585; NID:9236048; PIDN:AA819916.1; PID:9236049  
 R:Fabre, P.W.; King, A.; van Rooij, H.C.J.; Brinkmann, A.O.; de Boeth, N.J.; Trapman, J.  
 R:Chem. J. 278, 269-278, 1991  
 A:Title: The mouse androgen receptor. Functional analysis of the protein and characteriz  
 A:Reference number: S17198; MUID:91354214  
 A:Molecule type: DNA  
 A:Residues: 1-899 <FAZ>  
 A:Cross-references: EMBL:X59592; NID:949968; PIDN:CAA42160.1; PID:949969  
 A:Accession: S17198  
 A:Molecule type: mRNA  
 A:Residues: 1-899 <FAZ>  
 A:Cross-references: GB:X59592; NID:949968; PIDN:CAA42160.1; PID:949969  
 R:He, W.W.; Kumar, M.V.; Tindall, D.J.  
 Nucleic Acids Res. 19, 2373-2378, 1991  
 A:Title: A frame-shift mutation in the androgen receptor gene causes complete androgen  
 A:Reference number: S40626; MUID:91252278  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 366-413 <HEW>  
 A:Cross-references: EMBL:X53779  
 A:Molecule type: mRNA  
 A:Residues: 1-899 <RES>  
 Proc. Natl. Acad. Sci. U.S.A. 88, 8606-8610, 1991  
 A:Title: A single base deletion in the Tfm androgen receptor gene creates a short-lived  
 A:Reference number: 149501; MUID:92020902  
 A:Accession: I49501  
 A:Status: preliminary; translated from GB/EMBL/DDBJ

Query Match 15  
 Best Local Similarity 29.0%; Score 760; DB 2; Length 899;  
 Matches 223; Conservative 90; Mismatches 211; Indels 244; Gaps 25;  
 Qy 238 SPNAENRGSRSHSPAHASNNGSPL-----SSPLSSMKSSISSPPSHCSVKSPVSSPN 289  
 Db 61 SPRRRRQQHEDGSPQAHIRGPTGYLALEERQPSQQAASEGHPPESSCIEPEPGATA 120  
 A:Title: NYLRSSVSPANINNSRCSVSSPNTNNRSLTSSPASTVOSICSVNNAFSYTGS 349  
 Qy 290 NYLRSSVSPANINNSRCSVSSPNTNNRSLTSSPASTVOSICSVNNAFSYTGS 349  
 Db 121 GKGLPQOPAPPDDODDS-----AAPSTLSSLGP-----TPFGLS 154  
 Qy 350 AGSSTLRDVVPSPDT-----OEGKAQEVPPKTEEVESATNSGTVQLNIVOYIKPE 402  
 Db 155 SCSDAKDILNBEAGTMQLOQOOQOQHQHQHOHQHOHQOEVISEGGRAR-----EA 207  
 Qy 403 DGAFFS--SCLGGNSKNSDS-----SFSPVPIKQESTKHSCTSGTSFKGN----- 444  
 Db 208 TGAPSSSKDSYLGGSNTI-SDSAKELCKAVSVSMGLGVALEHLSPGEQLRGDCMVASL 266  
 Qy 445 ---PTVp-----FPMDGSFSFMKDQDKDVSLSLGLTGPPVPGFDNCES--- 487  
 Db 267 GGPPAVRPpPCAPLPECKGLPDEGPKSTEEPAEYSSFKGGYAKLEGESLGCGSSEA 326  
 Qy 488 -----GFPVQIKQEP-----GFPVQIKQEP----- 497  
 Db 327 GSSGTLIEPSSLSLYKSGALDEAAAYQNRRDYYNEPLALSGPBPBPPTPHARIKLENPL 386  
 Qy 498 DDGSYVYEA-----SIPSSATGVNNSG-----QSFR-----YRIGAQ 531  
 Db 387 DYGSAWAAAACQCRYGDLGLSHQGSVAGPSGSPATTSSWHTLFAEQEQLYGPQGG 446  
 Qy 532 TIS-----LSRSARDQSOIHL-----SSPPPVNL----- 556  
 Db 447 GSSSPSDAGPAPYGYTRPQGQTSQEDSASEWVWPGVVNRVPSPNCVKSEMPW 506  
 Qy 557 VESWKS HGD--LSSRSDGYPVLEYIPEWNSSSTLRSVSISSRSPSKICLVGDEASGC 613  
 Db 507 MENYSGPYGDMRLSDTRDHVLPIDYFP-----PQTKTCIGDABSGC 549  
 Qy 614 HYGVVTGCKFFKRAVEQGHNYLCAGRNDCDIDTRKKNPACRLQCLQAGMNIGA 673  
 Db 550 HRGALTGCKFFKRAEGOKYKLCSRNDCTIDKRRKNPSCRURKCYEAGMTIGR 609  
 Qy 674 KKKLGKLUIGIHEPOQOCQOPPPPPQSPERGTTYIAPEKEPSVNTALVPLFOLSTIR- 732  
 Db 610 KLUKLGNIK-LOE-----GENSNAGSPTEDPS-----OKMTVSHI 644  
 Qy 733 --ALTSPVMLENIPEIWAGYDSDSKPDAENLSTLNLAGKQMIQVWAKVLPG 789  
 Db 645 EGYECQPFLNLYLEIAEPGVVCAHGDNQQPSFAALLSSNLNEIGEROLVHVWKAALPG 704  
 Qy 790 FKNLPLEDQITLIQYSWMCISSEALSWRSYKHTNSQFLYFADPLVNE 837  
 Db 705 FRNLHVDQDMAVIQYSWMLGAMVAFMGWRSFTNVNSRMLYFADLVNE 752

Search completed: September 13, 2002, 10:16:58  
 Job time: 62 sec

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OM protein - protein search, using sw model

Run on: September 13, 2002, 10:17:01 ; search time 15.02 Seconds  
 (without alignments)  
 2178.297 Million cell updates/sec

Title: US-09-695-293-42  
 Perfect score: 4422  
 Sequence: 1 METKYHSLPEGLDMERRWG . . . . . FLYFAPDLYVNEELLARVREG 845

Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext: 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : SwissProt;40;\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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**SUMMARIES**

Result No.	Score	Query Match Length	DB ID	Description
1	43856	99.2	984	MCR_HUMAN
2	3985	90.1	984	MCR_TUPGB
3	3919.5	88.6	981	MCR_RAT
4	1763.5	39.9	612	MCR_XENLA
5	856	19.4	776	GCR_XENLA
6	856	19.4	777	GCR_HUMAN
7	854	19.3	776	GCR_TUPGB
8	853	19.3	777	GCR_ROTNA
9	850.5	19.2	771	GCR_CAVPO
10	847.5	19.2	703	GCR_PIG
11	845	19.1	777	GCR_SAGOE
12	842	19.0	783	GCR_MOUSE
13	841.5	19.0	795	GCR_RAT
14	840.5	19.0	778	GCR_SAISC
15	823	18.6	923	PRGR_RAT
16	814.5	18.4	758	GCR_ONCMY
17	806.5	18.2	807	1 GCR_PAROL
18	806	18.2	933	1 PRGR_HUMAN
19	805	18.2	786	PRGR_CHICK
20	804	18.2	923	1 PRGR_MOUSE
21	800	18.1	930	1 PRGR_RABIT
22	769	17.4	907	1 ANDR_CANFA
23	760	17.2	899	1 ANDR_MOUSE
24	759.5	17.2	377	1 PRGR_SHEEP
25	758.5	17.2	902	1 ANDR_RAT
26	751.5	17.2	884	1 ANDR_EULFC
27	738	16.7	895	1 ANDR_PAPHA
28	736	16.6	911	1 ANDR_PANTR
29	736	16.6	919	1 ANDR_HUMAN
30	736	16.6	919	1 ANDR_RABBIT
31	731.5	16.5	709	1 ANDR_RABIT
32	722	16.3	461.5	1 ESR1_XENLA
33	10.4		586	1 ESR1_XENLA

**RESULT 1**

ID	MCR_HUMAN	STANDARD;	PRT;	984 AA.
AC	P08235;	01-AUG-1988 (Rel. 08, Created)		
DT	01-AUG-1988	(Rel. 08, Last sequence update)		
DT	16-OCT-2001	(Rel. 40, Last annotation update)		
DE	Mineralocorticoid receptor (MR).			
GN	NR3C2 OR MLR OR MCR			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=87263386; PubMed=303703;			
RA	Arruda J.L., Weinberger C., Cerelli G., Glaser T.M., Handelin B.L., Housman D.E., Evans R.M.			
RT	"Cloning of human mineralocorticoid receptor complementary DNA: structural and functional kinship with the glucocorticoid receptor."			
RT	-!- FUNCTION: RECEPTOR FOR BOTH MINERALOCORTICOIDS (MC) SUCH AS ALDOSTERONE AND GLUCOCORTICOIDS (GC) SUCH AS CORTICOSTERONE OR CORTISOL. THE EFFECT OF MC IS TO INCREASE ION AND WATER TRANSPORT AND THUS RAISE EXTRACELLULAR FLUID VOLUME AND BLOOD PRESSURE AND LOWER POTASSIUM LEVELS.			
RT	-!- SUBCELLULAR LOCATION: Nuclear.			
RT	-!- DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN, A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.			
RT	-!- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY. NR3 SUBFAMILY.			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> or send an email to license@isb-sib.ch).			
CC	-----			
CC	EMBL: M18801; AAA55971.1; -.			
DR	PIR: A29513; A29513.			
DR	HSSP: P06536; IRGD.			
DR	TRANSFAC: T00513; -.			
DR	MIM: 600983; -.			
DR	PRINS: PR00047; STRIODEFINGER.			
DR	SMARC: SM00430; HOLI; 1.			
DR	InterPro: IPR000536; Hormone_rec_lig.			
DR	InterPro: IPR001628; zf-C4.			
DR	Pfam: PF00104; hormone_rec; 1.			
DR	Pfam: PF00105; zf-C4; 1.			
DR	PRINS: PR00047; STRIODEFINGER.			
DR	SMARC: SM00430; HOLI; 1.			
DR	PROSITE: PS00031; NUCLEAR RECEPTOR; 1.			
DR	Zinc finger; Steroid-binding MODULATING.			
FT	1			

P79373 macropus eu  
 P06212 gallus gall  
 Q91250 poephila gu  
 Q99315 mesocricetus  
 Q29040 sus scrofa  
 Q9tv98 equus cabal  
 P03372 homo sapien  
 P19785 mus musculus  
 P06211 rattus norvegicus  
 P57782 oncorhynchus  
 Q9jh32 oreochromis  
 Q62986 rattus norvegicus

FT	DNA_BIND	603	668	NUCLEAR RECEPTOR-TYPE.
FT	ZN_FING	623	623	C4-TYPE.
FT	DOMAIN	663	732	HINGE.
FT	SEQUENCE	984 AA:	107067 MW;	8300CD1A18C1858A CRC64;
Oy				
1	METKGYSLPEGLDMERRWQGQSAVERSSLGPTERTDENNYMEIVNVSCVSGAINNST	60		
1	METKGYSLPEGLDMERRWQGQSAVERSSLGPTERTDENNYMEIVNVSCVSGAINNST	60		
Db				
61	OGSSKEKQELPLCQLQDNRRPGILTSIKTELESKELSATVIESMGLYMDSYRDAYSYE	120		
61	OGSSKEKQELPLCQLQDNRRPGILTSIKTELESKELSATVIESMGLYMDSYRDAYSYE	120		
Db				
121	QQNQGSMSPAKIYQNVOLVKYKGNGHRPSTLSCNTPLASFMDSGSSYNGWRAI	180		
121	QQNQGSMSPAKIYQNVOLVKYKGNGHRPSTLSCNTPLASFMDSGSSYNGWRAI	180		
Db				
181	VKSPIMCHBKSPVSCPLMTSSVSCPAGINSVSTAASFGSRPPVHSPIQTGTPLTCSPN	240		
181	VKSPIMCHBKSPVSCPLMTSSVSCPAGINSVSTAASFGSRPPVHSPIQTGTPLTCSPN	240		
Db				
241	AENGRSRSHSPAHNSVNPSSPLSSMKSSTSSPPSICSVSPVSSNNVTLRSSVSSP	300		
241	AENGRSRSHSPAHNSVNPSSPLSSMKSSTSSPPSICSVSPVSSNNVTLRSSVSSP	300		
Db				
301	ANTINNSRCVSSPNTNRSTLSSPAASTVGSCSPVNNAFSYTAGSISAGSSTLRDVWP	360		
301	ANTINNSRCVSSPNTNRSTLSSPAASTVGSCSPVNNAFSYTAGSISAGSSTLRDVWP	360		
Db				
361	SPDQEKGQAEVPKTEVESASANGTGQNLNQVTKPEPGAFSSCLGNNSKIND	420		
361	SPDQEKGQAEVPKTEVESASANGTGQNLNQVTKPEPGAFSSCLGNNSKIND	420		
Db				
481	SFSPVPIKOSTKISCSGTSFKGPTVNPFPMGSYTFMDKDYSLSGIIGPPVGF	480		
421	SSFSVPIKESTKISCSCSFKGPTVFNFPMGSYFSFMDDKDYSLSLGGILGPPVGF	480		
481	DGNGEGSGFPVGITQEPDGSSYFEASIPSSATVGVNNSGQSFHYRAGQTISLSRAR	540		
481	DGNCGGSGFPVGIKOERPDGSSYFEASIFSSAIYGVNSGQSFHYRAGQTISLSRAR	540		
Db				
541	DOSFHLSSPPVNVILVEWSKSHDLSSRSRDGPVLETPENNSSTSRSVSTGSSRPS	600		
541	DOSFHLSSPPVNVILVEWSKSHDLSSRSRDGPVLETPENNSSTSRSVSTGSSRPS	600		
Db				
601	KICLYCGDEASCGHVGWTCGSCCKVFKAVEGHNLYCAGRNDCIIDKIRRKCPAQL	660		
601	KICLYCGDEASCGHVGWTCGSCCKVFKAVEGHNLYCAGRNDCIIDKIRRKCPAQL	660		
Db				
661	QKCLQAGMNIGARKSKKLKGKLGHEQQQQQPPPPPPQSEEGTYIAPKEPSN	720		
661	QKCLQAGMNIGARKSKKLKGKLGHEQQQQQPPPPPPQSEEGTYIAPKEPSN	720		
Db				
721	TALVPLSITSLAFLPSPVAVLENTEPELVYAGDSSKPDATENLSTLNLAGKOMIV	780		
721	TALVPLSITSLAFLPSPVAVLENTEPELVYAGDSSKPDATENLSTLNLAGKOMIV	780		
Qy				
781	VKWA KVLPGLPKNLPLPEDIQILOVYWNCLSSFA LSWRSYKHTNSOFLYAPDLVNE	837		
781	VKWA KVLPGLPKNLPLPEDIQILOVYWNCLSSFA LSWRSYKHTNSOFLYAPDLVNE	837		
Db				
Qy				
1	METKGYSLPEGLDMERRWQGQSAVERSSLGPTERTDENNYMEIVNVSCVSGAINNST	60		
1	METKGYSLPEGLDMERRWQGQSAVERSSLGPTERTDENNYMEIVNVSCVSGAINNST	60		
Db				
61	OGSSKEKQELPLCQLQDNRRPGILTSIKTELESKELSATVIESMGLYMDSYRDAYSYE	120		
Oy				
1	METKGYSLPEGLDMERRWQGQSAVERSSLGPTERTDENNYMEIVNVSCVSGAINNST	60		
1	METKGYSLPEGLDMERRWQGQSAVERSSLGPTERTDENNYMEIVNVSCVSGAINNST	60		
Db				
61	OGSSKEKQELPLCQLQDNRRPGILTSIKTELESKELSATVIESMGLYMDSYRDAYSYE	120		
Qy				
1	METKGYSLPEGLDMERRWQGQSAVERSSLGPTERTDENNYMEIVNVSCVSGAINNST	60		
1	METKGYSLPEGLDMERRWQGQSAVERSSLGPTERTDENNYMEIVNVSCVSGAINNST	60		
Db				
AC				
Q29131; Q95268;	STANDARD;	PRT;	977 AA.	
RESULT	2			
MCR_TUPGB				
ID				
AC				

DB	61 QESSKERQELIPCLQDNTQSGLTSEKTELEPKELSATVAESMGLYMDSVREADYAEE	RN [2]
OY	121 QONQGSMSPAKIYQNYEQOLVFKYKGNGHRSTLSCNTPLRSFMDSDGSSYNGGMRAI	SEQUENCE OF 689-787 FROM N.A.
DB	121 QHQAQESLSPARIKYQNYEQOLVFKYKGNGHRSTLSCNTPLRSFMDSDGSSYNGGMRAI	RE STRAIN-WISTAR; TISSUE-cochlea;
OY	181 VKSPIMCHEKSPVSQCSPLNMISVSGSAGMNSVSPASFSPPVHSPIOTPLCSPN	RX MEDLINE-9507883; PubMed-7992810;
DB	181 VKSPILCHEKSPVSQCSPLNMISVSGSAGMNSVSPASFSPPVHSPIOTPLCSPN	RX Furuta H., Mori N., Sato C., Hoshikawa H., Sakai S., Iwakura S., RA
OY	241 AENRGSRSHSAHASVNGPSLPISSPLSMKSSISSPSPHCYSKSPVSPNPNYLRSVSSP	RT "Mineralocorticoid type I receptor in the rat cochlea: mRNA identification by polymerase chain reaction (PCR) and in situ hybridization.";
DB	241 VDNRGSRSHSAHASVNGPSLPISSPLSMKSSISSPSPHCYSKSPVSPNPNYLRSVSSP	RT Hear. Res. 78:175-180(1994).
OY	301 ANINNSRCSVSSPNTNRSLSPLSPAASVGSICSVNNASVYTASCTAGSSTLRDVVP	RN [3]
DB	301 ANINNSRCSVSSPNTNRSLSPLSPAASVGSICSVNNASVYTASCTAGSSTLRDVVP	SEQUENCE OF 597-679 FROM N.A., AND ALTERNATIVE SPlicing.
OY	421 SSF-SPIKQESTKHSCKGSKRFGKGNPVINPPFDGDSYFSPMDKDYLSLGSILGPVPG	RT TISSUE=Brain;
DB	421 SSF-SPIKQESTKHSCKGSKRFGKGNPVINPPFDGDSYFSPMDKDYLSLGSILGPVPG	RT RX MEDLINE-9610549; PubMed-7495694;
OY	419 SPFSSVPVIQKQESTKHSCKGSKRFGKGNPVINPPFDGDSYFSPMDKDYLSLGSILGPVPG	RA Pratt J.H., Guo C., Pratt J.H.;
DB	419 SPFSSVPVIQKQESTKHSCKGSKRFGKGNPVINPPFDGDSYFSPMDKDYLSLGSILGPVPG	RT Identification of a splice variant of the rat and human mineralocorticoid receptor genes";
OY	480 FDGNCRGSGFPVGKIKOPPDGSYVPEASIPSSAIVGVNNGGOSFHRRIGAOCTISLRS	RL Steroid Biochem. Mol. Biol. 55:159-162(1995).
DB	480 FDGNCRGSGFPVGKIKOPPDGSYVPEASIPSSAIVGVNNGGOSFHRRIGAOCTISLRS	CC -1- FUNCTION: RECEPTOR FOR BOTH MINERALOCORTICOIDS (MC) SUCH AS ALDOSTERONE AND GLUCOCORTICOIDS (GC) SUCH AS CORTICOSTERONE OR CORITOL. THE EFFECT OF MC IS TO INCREASE ION AND WATER TRANSPORT AND THUS RAISE EXTRACELLULAR FLUID VOLUME AND BLOOD PRESSURE AND LOWER POTASSIUM LEVELS.
OY	479 FEGNCBGTGFFMGKIKOPPDGYIYPEASIPSSAIVGVNNGGOSFHRRIGAOCTISLRS	CC -1- SUBCELLULAR LOCATION: Nuclear.
DB	479 FEGNCBGTGFFMGKIKOPPDGYIYPEASIPSSAIVGVNNGGOSFHRRIGAOCTISLRS	CC -1- ALTERNATIVE PRODUCTS: TWO FORMS OF THE RECEPTOR ARE PRODUCED BY ALTERNATIVE SPLICING.
OY	540 RDOSFQHLSPPVNLVSEKSHGDLSSRASDGYPYLEIPENNSSTLAVSYGSSRP	CC -1- DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN, A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.
DB	540 RDOSFQHLSPPVNLVSEKSHGDLSSRASDGYPYLEIPENNSSTLAVSYGSSRP	CC -!- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
OY	598 SKICLIVCGDEASGCHGVWVTCGCKUFFKRAVEQOHNLACGRNDCIDKRRKNPACR	CC NR3 SUBFAMILY.
DB	598 SKICLIVCGDEASGCHGVWVTCGCKUFFKRAVEQOHNLACGRNDCIDKRRKNPACR	CC
OY	599 LQKLCLOGMGNLARKSKKLKGKLGHLREQPOQ-----PPPQSPPEGTYIAPAKEPSV	CC
DB	599 LQKLCLOGMGNLARKSKKLKGKLGHLREQPOQ-----PPPQSPPEGTYIAPAKEPSV	CC
OY	720 NTALVPLSITSLRALTSPSPAVLENTEPEPVYAGYSSKPDPAENLSTLNLAKGKOMIQ	CC
DB	720 NTALVPLSITSLRALTSPSPAVLENTEPEPVYAGYSSKPDPAENLSTLNLAKGKOMIQ	CC
OY	713 NTALVPLSITSLRALTSPSPAVLENTEPEPVYAGYSSKPDPAENLSTLNLAKGKOMIQ	CC
DB	713 NTALVPLSITSLRALTSPSPAVLENTEPEPVYAGYSSKPDPAENLSTLNLAKGKOMIQ	CC
OY	780 VVKWAKVLPGKNUPLQDQILOQSYWMCFLSSFALSFRSKYHTNSOFLYFADLVNE	CC
DB	780 VVKWAKVLPGKNUPLQDQILOQSYWMCFLSSFALSFRSKYHTNSOFLYFADLVNE	CC
OY	837 773 VVKWAKVLPGKNUPLQDQILOQSYWMCFLSSFALSFRSKYHTNSOFLYFADLVNE	CC
DB	837 773 VVKWAKVLPGKNUPLQDQILOQSYWMCFLSSFALSFRSKYHTNSOFLYFADLVNE	CC
RESULT	3	CC
MCR_RAT	MCR_RAT	CC
ID	MCR_RAT	CC
AC	P22199; 063763; 064174;	CC
DT	01-AUG-1991 (Rel. 19, Created)	CC
DT	01-AUG-1991 (Rel. 19, Last sequence update)	CC
DT	01-MAR-2002 (Rel. 41, Last annotation update)	CC
DE	Mineralocorticoid receptor (MR).	CC
GN	NR3C2 OR MR.	CC
OS	Rattus norvegicus (Rat).	CC
OC	Bukarriota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.	CC
OX	NCBI_TAXID=10116; [1]	CC
RN	SEQUENCE FROM N.A.	CC
RC	STRAIN="SPRAGUE-DAWLEY; TISSUE=Hippocampus;	CC
RX	MLINE="9014194; PubMed-255305;	CC
RT	Patel P.D., Sherman T.G., Goldman D.J., Watson S.J.;	CC
RT	"Molecular cloning of a mineralocorticoid (type I) receptor complementary DNA from rat hippocampus.";	CC
RL	Mol. Endocrinol. 3:1877-1885(1989).	CC
RP	Query Match 88.6%; Score 3919.5; DB 1; Length 981; Best Local Similarity 89.0%; Pred. No. 2.4e-200; Matches 746; Conservative 35; Mismatches 52; Indels 5; Gaps 2; Sequence 981 AA; 106737 MW; 184F5D37C1B030F7 CRC64;	CC
OY	1 METRGYHSLPEGLDERRNGQSYQANVERSSLGPTERIDENNMEIVNVSCVSGAIPNNST	CC

Db 1 METKGYHSPEGLDMERRWSQSVQSTLERSIGPAERTTENNYNETIVNSCVSGAIPNNT 60 CC  
 QY 61 QGSKREKOKILPCHQDNNRPGITTSIDTKTELESKELSATVAESMGLYMDSYRDAYS 120 CC  
 Db 61 QGSSKEKHELLPTIQODNSRSRGLPSDKTELESKELSATVAESMGLYMDSYRDAETD 120 CC  
 -1- DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN.  
 Db 121 QONOOGSMSPAKTYONVOLVKFVKNGHRPSTISCVNPLRSFMSDSGGSSYNGVMRAI 180 CC  
 QY 121 QONOOGSLSPLTKIYONMEOLVKFYKENGHRSSILSAMSRPLRSFFMPDSAASMGALRAI 180 CC  
 Db 181 VKSPIMCHAKPSVCSPLINTSSCSPAGINSYSTASFGSPPVHHSITOGPLTCSPN 240 CC  
 QY 181 VKSPIMCHAKPSVCSPLINTSSCSPAGINSYSTASFGSPPVHHSITOGPLTCSPN 240 CC  
 Db 241 AENRGSRSHSPASHAVNGVPLSSLSMKSISPPSHCSVKPFVSSNNVLRSSVSP 300 CC  
 QY 241 VENGRSRSHSPATHASNNGVPLSSLSSMKSISPPSHCSVKPFVSSNNVLRSSVSP 300 CC  
 Db 301 ANTINNSRCVSPPSNTNNRSTLSSPAASTVGSTICSPVNNAFSYTAGSTSAGSSTLRDV 359 CC  
 QY 301 ANTINNSRCVSPPSNTNNRSTLSSPAASTVGSTICSPVNNAFSYTAGSTSAGSSTLRDV 359 CC  
 Db 360 PSPDQIPEQKGAQEVPIPKTERVESALSGNYTGQLNIVQYKPEPGAFSSCLGGNSKIN 419 CC  
 QY 360 PSPDQIPEQKGAQEVPIPKTERVESALSGNYTGQLNIVQYKPEPGAFSSCLGGNSKIN 419 CC  
 Db 361 PSPDTHEKGAHDVPPKTERVEKAISNGVTGPLNIVQYKSEPGAFSSCLGGNSKIN 420 CC  
 QY 420 DSSFSVPIKQESTKSCSGSFKQMPVTVPFPMDGSYFSFMDDKDYSLSGTGPPYVG 479 CC  
 Db 421 SSPFSVPIKOBSSKHSGASFKGNPTVNPFPMDGSYFSFMDDKDYSLSGTGPPYVG 480 CC  
 QY 480 FDGNCCEGSGPPVGKIQEPDGSSYTFEASIPSAIVGYNSSGQSPHYRGAQGTSLNSA 539 CC  
 Db 481 FDGSCEDSAPVGTKIOPDGSYTFEASIPSAIVGYNSSGQSPHYRGAQGTSLNSRSP 540 CC  
 QY 540 RDQSFQHLSRSPVNLVSEWKSHDLSRSRSDGYPVLEYIPEVNSSSLRSVSTGSSRP 599 CC  
 Db 541 RDQSFQHLSRSPVNLVSEWKSHDLSRSRSDGYPVLEYIPEVNSSSLRSVSTGSSRP 600 CC  
 Qy 600 SKICLVCGDEASGCHYGVTCGSKCKVFKKAVEGOHNLYCAGRNDCCIDKIRRNCPACR 659 CC  
 Db 601 SKICLVCGDEASGCHYGVTCGSKCKVFKKAVEGOHNLYCAGRNDCCIDKIRRNCPACR 660 CC  
 Qy 660 LOKCLOAGMNUGARSKKKLGKLGHFEEQQQQQPPPPPOPOPEEGTYIAKERSV 719 CC  
 Db 661 LOKCLOAGMNUGARKSKKLGLKLGHFEEQQOO---PPPPPOQSPPEEGTYIAKERSV 716 CC  
 Qy 720 NIALVNPOLISTISRALTPSPVWLENTEPEIYAGTDSSKDTAENIUSTLNLAGKOMIQ 779 CC  
 Db 717 NSALVPOLISTISRALTPSPVWLENTEPEIYAGTDSSKDTAENIUSTLNLAGKOMIQ 776 CC  
 Qy 780 VVKWAKVLPGEFKNLPLEDQITIYQSWMCILSFFALSWSRSYKHTNSQFLYFADLVNE 837 CC  
 Db 777 VVKWAKVLPGEFKNLPLEDQITIYQSWMCILSFFALSWSRSYKHTNSQFLYFADLVNE 834 CC  
 RESULT 4  
 MCR\_XENLA ID MCR\_XENLA STANDARD; PRT; 612 AA.  
 AC 091573; 091723; 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 01-MAR-2002 (Rel. 41, Last annotation update)  
 DE Mineralocorticoid receptor (MR) (Fragment).  
 GN NR3C2 OR MR.  
 OS Xenopus laevis (African clawed frog).  
 OC Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea;  
 OC Xenopodidae; Xenopus.  
 NCBI\_TAXID: 3355;  
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 RP SEQUENCE FROM N.A.; Danielssen M.;  
 RA Csikos T., Tay J., Danielssen M.;  
 RL Submitted (SEP-1995) to the EMBL/GenBank/DDBJ databases.

Query Match 39,9%; Score 1763,5; DB 1; Length 612;  
 Best Local Similarity 72,1%; Pred. No. 1,7e-86; Matches 57; Indels 23; Gaps 8;  
 Matches 338; Conservative 57; Mismatches 51;

Db 392 LNIYVYIKPEPDGFASSCIGGNSKINDSSFSVPIKOSTKHSCTSGTSFKGNPTVWFP 451  
 QY Db 9 VSLVIFKIDPDAFSSICFG--DTVSSDPAFSIPKQESCKTCSSALFKGSOSANRFP 66  
 QY Db 452 FMDGSYFSFMDKDYYSLSGILGPVPGDFDNGCEGSGP---VGKQEPDGSSYPEA 506  
 QY Db 67 FMDGSYFAFMDDKDYSLSGILGPVSSFGDFEGNGFSNQSLNVAQTEDSSTVFN 126  
 QY Db 507 SIPSSAIVGNSGGOSPHYRIGAGTISRSA-RDOSRHOHSFPPVNTLWESWKHGD 565  
 Db 127 NMPSSAIVGVNSCGSOSPHYRIGAQTISRSA-RDOSRHOHSFPPVNTLWESWKHGD 566  
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 Db 187 LAQNTLSSRNDGFVPGYIPEVNSSSLRSVSGSSRPSKICLVCGDEASGCHYGVTC 246  
 QY 621 GSCKVFKRAVEG---OHNYLCAGRNDCTIDKTRKNCPACRQLCQAGMNUGARKSK 676  
 Db 247 GSCKVFKRAVEGCKSRQHNSYLCAGRNDCTIDKIRRNCPACRQLCQAGMNUGARKSK 306  
 QY 677 KLGKKGIGHEQQQQPPPPPPQSPEREGTTIAPAKEPSNT-ALVVPOLSTISRALT 735  
 Db 307 KLGKKGIGHEQQQQPPPPPPQSPEREGTTIAPAKEPSNT-ALVVPOLSTISRALT 735  
 QY 736 PSPVWLENTEPEIYAGTDSSKDTAENIUSTLNLAGKOMIQVKAKVLPGFKNPL 795  
 Db 364 LSAAVILENTEPEIYAGTDSSKDTAENIUSTLNLAGKOMIQVKAKVLPGFKNPL 423



- OS Homo sapiens (Human);  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
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 RP SEQUENCE FROM N.A.  
 RX MEDLINE=86092206; PubMed=2867473;  
 RA Hollenberg S.M., Weinberger C., Ong E.S., Cerelli G., Oro A.,  
 Lebo R., Thompson D., Rosenfeld M.G., Evans R.M.;  
 RT "Primary structure and expression of a functional human  
 glucocorticoid receptor cDNA.";  
 RL Nature 318:635-641(1985).  
 RN [2]  
 RP SEQUENCE FROM N.A. (ISOFORMS ALPHA AND BETA).  
 RX MEDLINE=91201378; PubMed=1707081;  
 RA Encio I.J., Detera-Wadleigh S.D.;  
 RT "The genomic structure of the human glucocorticoid receptor.";  
 RL J. Biol. Chem. 266:1827-1881(1991).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA Munroe D.G., Pang J., Taylor G.R., Lau C., Plante R.K., Zhou L.;  
 RL Submitted (SEP-1993) to the EMBL/genBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE OF 1-394 FROM N.A.  
 RX MEDLINE=91224961; PubMed=2020589;  
 RA Leclerc S., Xie B.X., Roy R., Govindan M.V.;  
 RT "Purification of a human glucocorticoid receptor gene promoter-binding  
 protein. Production of polyclonal antibodies against the purified  
 factor.";  
 RL J. Biol. Chem. 266:8711-8719(1991).  
 RN [5]  
 RP SEQUENCE OF 396-630 FROM N.A.  
 RA Kimerly W., Bondoc M., Cheng J., Connolly K.S., Gunning K.M.,  
 RA Kadner K., Miguel T., Miller C., Pitluck S., Pollard M., Rojeski H.,  
 RA Subramanian S., Martin C.H.;  
 RL Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.  
 RN [6]  
 RP DOMAINS.  
 RX MEDLINE=90092211; PubMed=3841189;  
 RA Weinberger C., Hollenberg S.M., Rosenfeld M.G., Evans R.M.;  
 RT "Domain structure of human glucocorticoid receptor and its  
 relationship to the v-erb-A oncogene product.";  
 RL Nature 318:670-672(1985).  
 RN [7]  
 RP VARIANT SER-363.  
 RX MEDLINE=93181003; PubMed=8445027;  
 RA Karl M., Lamberts S.W.J., Detera-Wadleigh S.D., Encio I.J..  
 RA Stratakis C.A., Hurley D.M., Accili D., Chrousos G.P.;  
 RT "Familial glucocorticoid resistance caused by a splice site deletion  
 in the human glucocorticoid receptor gene.";  
 RL J. Clin. Endocrinol. Metab. 76:683-689(1993).  
 RN [8]  
 RP VARIANT VAL-641.  
 RX MEDLINE=91123468; PubMed=1704018;  
 RA Hurley D.M., Accili D., Stratakis C.A., Karl M., Vamvakopoulos N.,  
 RA Rorer E., Constantine K., Taylor S.I., Chrousos G.P.;  
 RT "Point mutation causing a single amino acid substitution in the  
 hormone binding domain of the glucocorticoid receptor in familial  
 glucocorticoid resistance.";  
 RL J. Clin. Invest. 87:680-686(1991).  
 RN [9]  
 RP VARIANT ILE-729.  
 RX MEDLINE=93253031; PubMed=7683692;  
 RA Malchoff D.M., Brusky A., Reardon G., McDermott P., Javier E.C.,  
 RA Bergh C.H., Rowe D., Malchoff C.D.;  
 RT "A mutation of the glucocorticoid receptor in primary cortisol  
 resistance.;"  
 RL J. Clin. Invest. 91:1918-1925(1993).  
 RN [10]  
 RP VARIANT PHE-753.  
 RX MEDLINE=93302771; PubMed=8316249;  
 RA Asnaf J., Thompson E.B.;  
 RT "Identification of the activation-labile gene: a single point mutation  
 in the human glucocorticoid receptor presents as two distinct receptor  
 phenotypes.";  
 RT Ruiz M., Lind U., Gafveus M., Eggertsen G., Carlstedt-Duke J.,  
 RA Nilsson L., Holtermann M., Stierna P., Wikstrom A.C., Werner S.;  
 RL Mol. Endocrinol. 7:631-642(1993).  
 RN [11]  
 RP VARIANTS HIS-477 AND SER-679.  
 RX PubMed=11589680;  
 RA Ruiz M., Lind U., Gafveus M., Eggertsen G., Carlstedt-Duke J.,  
 RA Nilsson L., Holtermann M., Stierna P., Wikstrom A.C., Werner S.;  
 RT "Characterization of two novel mutations in the glucocorticoid  
 receptor gene in patients with primary cortisol resistance.";  
 RL Clin. Endocrinol. (oxf) 55:363-371(2001).  
 CC -!- FUNCTION: THE STEROID HORMONES AND THEIR RECEPTORS ARE INVOLVED IN  
 CC THE REGULATION OF EUKARYOTIC GENE EXPRESSION AND AFFECT CELLULAR  
 CC PROLIFERATION AND DIFFERENTIATION IN TARGET TISSUES. BINDS TO THE  
 CC GRE TARGET SITE.  
 CC -!- SUBCELLULAR LOCATION Nuclear.  
 CC PRODUCED BY ALTERNATIVE PRODUCTS: 2 ISOFORMS; ALPHA (SHOWN HERE) AND BETA; ARE  
 CC PHYSIOLOGICAL FORM OF HGR. THE IN VITRO TRANSLATION PRODUCT OF HGR  
 CC BETA DOES NOT BIND STEROID. ITS FUNCTION IS UNCLEAR; HOWEVER, IT IS  
 CC POSSIBLE THAT VARIANT RECEPTORS PERFORM TISSUE-SPECIFIC FUNCTIONS.  
 CC -!- DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN,  
 CC A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.  
 CC -!- DISEASE: DEFECTS IN NR3C1 ARE A CAUSE OF FAMILIAL GLUCOCORTICOID  
 CC RESISTANCE (CORTISOL RESISTANCE); A HYPERTENSIVE, HYPERANDROGENIC  
 CC DISORDER CHARACTERIZED BY INCREASED SERUM CORTISOL CONCENTRATIONS.  
 CC -!- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.  
 CC NR3 SUBFAMILY.  
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 DR EMBL; U78748; AAB64354.1; JOINED.  
 DR EMBL; U78749; AAB64354.1; JOINED.  
 DR EMBL; U78750; AAB64354.1; JOINED.  
 DR EMBL; U78751; AAB64354.1; JOINED.  
 DR EMBL; U78752; AAB64354.1; JOINED.  
 DR EMBL; U78753; AAB64354.1; JOINED.  
 DR EMBL; U78754; AAB64354.1; JOINED.  
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 DR EMBL; U78757; AAB64354.1; JOINED.  
 DR EMBL; U78758; AAB64354.1; JOINED.  
 DR EMBL; U78759; AAB64354.1; JOINED.  
 DR EMBL; U78760; AAB64354.1; JOINED.  
 DR EMBL; U78761; AAB64354.1; JOINED.  
 DR EMBL; U78762; AAB64354.1; JOINED.  
 DR EMBL; U78763; AAB64354.1; JOINED.  
 DR EMBL; U78764; AAB64354.1; JOINED.  
 DR EMBL; U78765; AAB64354.1; JOINED.  
 DR EMBL; U78766; AAB64354.1; JOINED.  
 DR EMBL; U78767; AAB64354.1; JOINED.  
 DR EMBL; U78768; AAB64354.1; JOINED.  
 DR EMBL; U78769; AAB64354.1; JOINED.  
 DR EMBL; U78770; AAB64354.1; JOINED.  
 DR EMBL; U78771; AAB64354.1; JOINED.  
 DR EMBL; U78772; AAB64354.1; JOINED.  
 DR EMBL; U78773; AAB64354.1; JOINED.  
 DR EMBL; U78774; AAB64354.1; JOINED.  
 DR EMBL; U78775; AAB64354.1; JOINED.  
 DR EMBL; U78776; AAB64354.1; JOINED.  
 DR EMBL; U78777; AAB64354.1; JOINED.  
 DR EMBL; U78778; AAB64354.1; JOINED.  
 DR EMBL; U78779; AAB64354.1; JOINED.  
 DR EMBL; U78780; AAB64354.1; JOINED.  
 DR EMBL; U78781; AAB64354.1; JOINED.  
 DR EMBL; U78782; AAB64354.1; JOINED.  
 DR EMBL; U78783; AAB64354.1; JOINED.  
 DR EMBL; U78784; AAB64354.1; JOINED.  
 DR EMBL; U78785; AAB64354.1; JOINED.  
 DR EMBL; U78786; AAB64354.1; JOINED.  
 DR EMBL; U78787; AAB64354.1; JOINED.  
 DR EMBL; U78788; AAB64354.1; JOINED.  
 DR EMBL; U78789; AAB64354.1; JOINED.  
 DR EMBL; U78790; AAB64354.1; JOINED.  
 DR EMBL; U78791; AAB64354.1; JOINED.  
 DR EMBL; U78792; AAB64354.1; JOINED.  
 DR EMBL; U78793; AAB64354.1; JOINED.  
 DR EMBL; U78794; AAB64354.1; JOINED.  
 DR EMBL; U78795; AAB64354.1; JOINED.  
 DR EMBL; U78796; AAB64354.1; JOINED.  
 DR EMBL; U78797; AAB64354.1; JOINED.  
 DR EMBL; U78798; AAB64354.1; JOINED.  
 DR EMBL; U78799; AAB64354.1; JOINED.  
 DR EMBL; U78800; AAB64354.1; JOINED.  
 DR EMBL; U78801; AAB64354.1; JOINED.  
 DR EMBL; U78802; AAB64354.1; JOINED.  
 DR EMBL; U78803; AAB64354.1; JOINED.  
 DR EMBL; U78804; AAB64354.1; JOINED.  
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 DR EMBL; U78806; AAB64354.1; JOINED.  
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 DR EMBL; U78811; AAB64354.1; JOINED.  
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 DR EMBL; U78815; AAB64354.1; JOINED.  
 DR EMBL; U78816; AAB64354.1; JOINED.  
 DR EMBL; U78817; AAB64354.1; JOINED.  
 DR EMBL; U78818; AAB64354.1; JOINED.<

DR	SMART: SM00430; HOLE: 1.
DR	SMART: SM00399; Znf_C4: 1.
DR	PROSITE: PS00031; NUCLEAR_RECEPTOR: 1.
KW	Receptor; Transcription regulation; DNA-binding; Nuclear Protein; Zinc-finger; Steroid-binding; Disease mutation; Polymorphism;
KW	Alternative splicing; DOMAIN_1: 420
FT	DNA_BIND: 421
FT	ZN_FING: 421
FT	ZN_FING: 457
FT	ZN_FING: 481
FT	DOMATN: 487
FT	DOMAIN: 528
FT	VARSPLC: 728
FT	VARIANT: 363
FT	VARIANT: 477
FT	VARIANT: 641
FT	VARIANT: 679
FT	VARIANT: 729
FT	VARIANT: 753
FT	CONFFLICT: 451
SQ	SEQUENCE: 777 AA;
Query Match	19.4%; Score 856; DB 1; Length 777;
Best Local Matches	35.0%; Pred. No. 2.4e-38; Mismatches 239; Conservative 83; Indels 212; Gaps 25;
Qy	248 SHSPAHASNYGSPPISSPPLSSMKSSISSPSPHSCKSVKSPVSSPPNNVTLSRSPSSPANINNSR 307
Db	6 SLTPGREENSSVLAQERGVMDYFKTLRGATKVVSASSPS---LAVASQDSKQR 60
Qy	308 CSVSSPSNTNRS--TLSSPAASSTVG----SCSPVNNAFSYTAGS--TSGSSTLR 356
Db	61 LIVDPFPKGSKVSNAAQPDLSKAVSISMGLYMGETETRVMGNDLGPPOQQQISLSETDLSK 120
Qy	357 DVVPS-----PDTOBKGAQ-----EVPPPKTEEEVSAISNGYTQQLNIVQYI 398
Db	121 LLEESIANLNRSNSTVSPNPKSAASVAAPEERKPKHHSVDSSEQHQHKQ----- 173
Qy	399 KPEPDGAFSSCLGNISKI--NSISFFSV-----PIKQESTKHSCTSGTSFKGNPT 446
Db	174 -----TGTNGSGNVNLKTYDOSTFDIQLDFLFRSSGSGPKETINESPWRSIDLIDENCL 224
Qy	447 VNPFPEFMDSYF-----SEMPDKDY--SLSGILGPVPGDGNC 485
Db	225 LSPAGEDDFSLLLEGNSNEDECKPLLPDTKPKIKDGLVLSSPSNTLPQV---KTE 279
Qy	486 GSGF----PGIKOEPDGDYVPEAISPAVNG-----VNSGQSFHYRIGA 529
Db	280 KEDFIELCTPGVIKKG-KLGTVYCOASPGCANITGNKMSAISVHGVTSGOMWHDM-- 336
Qy	530 QGTTSLSRSARDQSFOHLSSPPVNTLVEW--KSHGD--LSSRRSDGVPLEYIPENV 584
Db	337 -NTASLSQQ-QDQK-PIFNVIPIPVGSEWNRRCGSGDDNLTSGLTNFPGRTVFSNGY 393
Qy	585 SSSTLER-----SYSTGSS-RPSKICLVCGDDEASGCHGHWVCGSKVFFKRAVEQH 635
Db	394 SSPSMRHPDVSSPPSSSSTAATGPPPKLCLVCSDEASGCHGVLTGCGSKVFFKRAVEQH 453
Qy	636 NYLCAGRNDCIDKIRRKNPACRQLCOKCLOGMNLGARKSKKLKGKLGHEBQPOQQQP 695
Db	454 NYLAGRNDCIDKTRRKNPACRQLCOKCLOGMNLGARKSKKLKGKLGHEBQPOQQQP 504
Qy	696 PPPPPQQQSPEEGTVIAPAKEPSVNTALPVOLSTISRALTPSPWAVLENTEPEIYAGYD 755
Db	505 TGVSOETSENPGNKTTIVPATLPQ-----LTFPLVSLIEVEPEVLVAGYD 549
Query Match	19.3%; Score 854; DB 1; Length 776;
RESULT	7
GCR_TUPGB	ID
GCR_TUPGB	GCR_TUPGB
STANDARD	PRT:
	776 AA.
095267;	AC
01-NOV-1997 (Rel. 35, Created)	DT
16-OCT-2001 (Rel. 40, Last annotation update)	DT
NR3CL OR GR1.	DE
Tupaia glis belangeri (Common tree shrew).	GN
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Scandentia; Tupaidae; Tupaia.	OC
NCBI_Taxid=9396;	OX
[1]	RN
SEQUENCE FROM N_A.	RP
TISSUE=Brain;	RC
MEDLINE=9825005; PubMed=9582428;	RX
Meyer U., Flugge G., Fuchs E.; Meyer U., Kruhoefer M., Flugge G., Fuchs E.;	RA
"Cloning of glucocorticoid receptor and mineralocorticoid receptor mRNA and gene expression in the central nervous system of the tree shrew (Tupaia belangeri).";	RT
Brain Res. Mol. Brain Res. 55:243-253 (1998)	RL
- FUNCTION: THE STEROID HORMONES AND THEIR RECEPTORS ARE INVOLVED IN THE REGULATION OF EUKARYOTIC GENE EXPRESSION AND AFFECT CELLULAR PROLIFERATION AND DIFFERENTIATION IN TARGET TISSUES. BINDS TO THE GRE TARGET SITE.	CC
- SUBCELLULAR LOCATION: Nuclear.	CC
- DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN, A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.	CC
- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.	CC
NR3 SURPAMYLI.	CC
-----	CC
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-----	CC
EMBL; Z75079; CA99379.1; -.	DR
HSSP; P06536; IRED.	DR
InterPro; IPR01409; Glucocorticd.receptor.	DR
InterPro; IPR00536; Hormone_rec_lig.	DR
InterPro; IPR00628; zf-C4.	DR
Pfam; PF02155; GCR; 1.	DR
Pfam; PF00104; hormone_rec; 1.	DR
Pfam; PF00105; zf-C4; 1.	DR
PRINTS; PRO0047; STROIDFINGER.	DR
SMART; SM00430; HOLE: 1.	DR
SMART; SM00399; Znf_C4; 1.	DR
PROSITE; PS00031; NUCLEAR RECEPTOR; 1.	DR
Receptor; Transcription regulation; DNA-binding; Nuclear protein; Zinc-finger; Steroid-binding.	KW
Modulating.	FT
DNA_BIND: 420	FT
ZN_FING: 420	FT
ZN_FING: 456	FT
ZN_FING: 480	FT
DOMATN: 419	FT
SEQUENCE: 776 AA;	SQ
85837 MW;	SQ
972CICA2334C6058 CRC64;	SQ
776 AA;	SQ
19.3%; Score 854; DB 1; Length 776;	SQ

	Best Local Similarity	Pred NO.	Score	Length	DB	NO.
Matches	264;	Conservative	94;	Mismatches	222;	Indels
					278;	Gaps
QY	27	ERSSLGPTER-----IDENNMTIVN----SCVSGAIPNINSTOGSSKEKQELPCLQ	75		33;	
Db	4	KESLTPSPTEIPSSVYHGQQRRGVNMDYKTRGGATKVYFMPSPSIGSS-----Q	53			
QY	76	ODNNRPGILTSEDIK---TELESKESTATAEWSMGIM---DSYRADYSYEQQNQQGSM	128			
		:      :      :         :      :      :      :      :				
Db	54	SDSKOQLRLWDFFPKGSVSNWQDPLSKAVSLSMGLYMGEMETKYMNDLGFPOQGQ---	109			
QY	129	SPAKYIQYNEFOLVKFYKGCHRSPLTLCVNTPLRSFMSDGGSSVNGVMRAIKVSPIMCH	188			
	:      :      :      :      :      :      :      :					
Db	110	-----TLLSGEFTNLQ LLEESIANLN-----	130			
QY	189	EKSPSYCSPNMTSSVCSPAGINSVSSTASFGSPVHSIITQGTPLTCSPPNAENRGSR	248			
	:      :      :      :      :      :      :      :					
Db	131	-RTSIVPEHKISAYAVSAL-----	151			
QY	249	RSPAHASNVGSPPLSSPLSSMKSSISSPPSHCSVKSFPVSSNNVTSSPAN- NNSR	307			
	:      :      :      :      :      :      :      :					
Db	152	-----LKKELPTEPSDVSESEQNQULKQGQTG- GNVKLTADOSTFDLQDLE	198			
QY	308	CSVSSPSNTNRNSTLSSPAASTVGSCSPVNNAFSYTAQS-TAGSSTLRDVPSDTQE	367			
	:      :      :      :      :      :      :      :					
Db	199	FSSASPGRETNEESPWRSDLIDENCILSPL-----	228			
QY	368	GAQEVPFPKTEVEVASISNGTQGLNIWQYIKP- EPDGAFASSCLGGNNSKINSDSSFSV	425			
	:      :      :      :      :      :      :      :					
Db	229	AVEDDEP-----LSEG-----NLKEDCKPLLPD--TKPKIKDGDILLSPSPKN	271			
QY	426	PIKQUESTKHSCSGTSFKGNPTVNPFPMDSYFSFADDKDYLSLCLGPPVPGFENCE	485			
	:      :      :      :      :      :      :      :					
Db	272	PLPQVKT-----EKFDFIELC-----TPGV-----	291			
QY	486	GSGFPVGIKQERDDGSVYYPEASIPSSAIVG----- VNSGGOSFHVRIGAQTS	534			
	:      :      :      :      :      :      :      :					
Db	292	-----IKQE-KLGPVYCQAMFGANTIGNKMSAISVHGVSTGSGOMYHDM-- NTAT	340			
QY	535	LRSRARDPOSFQLLSSFPVNTLVESW-- KSHGD-----LSRRR- SDGYPYLE	579			
	:      :      :      :      :      :      :      :					
Db	341	LSQQ-QPQK- PTFNVIPIPVSSENWNRCQGGSDENLITSGLTINFSGRSVFSNGYSSPGM	398			
QY	580	IPENVSSSTLRSYSTGSSRPSKICLIVGDEASGHCHYCVTGCSCKVFKRAVEGORNLYC	639			
	:      :      :      :      :      :      :      :					
Db	399	RPD-VSSPPNSL-AVGPPPKFCVGSDEASGCHYCVTGCSCKVFKRAVEGORNLYC	456			
QY	640	AGRNDCITDKIREKNCFACRLQKLCQAGMNLGARKSKKLKGKIHEEQQQQPPPPP	699			
	:      :      :      :      :      :      :      :					
Db	457	AGRNDCTIEKIRKNCAPCRYRKCLQAGMLNLEARKTKK-- KTKGIQTTGISOETP--	511			
QY	700	PROSPEEGTYIAPAKERSVNTALVPLQSTISRALTPSPVMVIENTEPPIVAGYDSSKP	759			
	:      :      :      :      :      :      :      :					
Db	512	-----ENSANKTIIVP- ATLPQ- LTPPIFVSLLEVIEREVLYAGYDSSLP	552			
QY	760	DIAENLUSLTLNRAKGKOMIQWVAKWVLFGEKNUPLDQITLQYQSNMCILSSALWSRY	819			
	:      :      :      :      :      :      :      :					
Db	553	DTWRIMSAVLNMGGQRQVIAVKWAKAIEGFRNLHDDQMTLQYSWMELMAGLFWRSY	612			
QY	820	KHTNSQFLYFAPDLYNE	837			
	:      :      :      :      :      :      :      :					
Db	613	KQASANLICFAPDLINE	630			
RESULT	8					
GCR_AOTNA						
ID						
AC	P79886;					
DT	01-Nov-1997 ( Rel. 35, created)					
DT	01-Nov-1997 ( Rel. 35, last sequence update)					
DT	16-Oct-2001 ( Rel. 40, last annotation update)					
Glucocorticoid receptor (GR).	NR3C1 OR GRL.					
NR3C1						
Query Match	19.3%	Score	853;	DB	1;	Length
Best Local Similarity	30.5%	Pred.	No. 3	58-38;		
Matches	259;	Conservative	105;	Mismatches	224;	Indels
					262;	Gaps
						32;
QY	28	RSSLGGPTERDENNYM- ELYNNSCVSGAIPNINSTOGSSKEKOBILPCLQDNNRPGIL	85			
	:      :      :      :      :      :      :      :					
Db	4	KESLTPGKEENPSSVLTQERGVNMDFSKILRGGAATKVSVSSTSLAASQSDSKQQLIV	63			
QY	86	SDIK---TELESKESTATAEWSMGIM---DSYRADYSYEQQNQQGSMSPARTYQVNE	138			
	:      :      :      :      :      :      :      :					
Db	64	DFPKGSVSNQDPDSKAVSLSMGLYMGEMETKYMNDLGFPOQCOISLSGETDQLO	123			
QY	139	OLVKFYKGHRSPTLSVCVNTPLRSFMSDGGSSVNGVMRAIKVSPIMCHEKSFVCSL	198			
	:      :      :      :      :      :      :      :					
Db	124	ESI-----				ANL 129
QY	199	NMTSSVCSPAGINSVSSTASFGSPVHSIITQGTPLTCSPPNAENRGSRSHSPAHASNV	258			
	:      :      :      :      :      :      :      :					
Db	130	NRSTSVPE---NPKSASSSVSAAP-----KEKEFPTH-----	160			

QY	259 SPLSSPLSSMKSSISSPSPHSCSVKSPVSSPNNTLRSVSSPANI-NNSRCSVSSPNTN 317	CC	-!- DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN, A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.
Db	161 SDVSESEQONLKGQTG-----TNGCNVKLYTADOSTFDIQLDFESSPGKET 208	CC	-!- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
QY	318 NRSTLSSPAASTVOSICSPV-NNAFSYTSAGTSAGSSSTDRLWV--SPDQEKAQEVF 374	CC	NR3 SUBFAMILY.
Db	209 NQSPWKSDLIDENCLLSPLAGEEDSFLLLEGNSN---EDCKPLILPDK----- 254	CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation and the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> ) or send an email to licensee@ib-sib.ch).
QY	375 PKTEEVESATISNGVTGOLNIVQYKPEPDGFASCLGGNSKINSDSTSFSVP-IKQESTK 433	CC	CC
Db	255 PKIKD----- 280	CC	CC
QY	494 KQEPDDGSYYPEASIPSSAIVG-----VNSGGOSFHYRIGAQGTISLSRSARDQ 542	CC	CC
QY	434 HSCSGTSFKGNPTVNPFPMDGSYFSFMDKDYSLSGITLGPPGFDGNCCEGSPFPVG 493	CC	CC
Db	281 -----EDFIELD-----TPGV-----I 292	CC	CC
QY	543 SFQHLSFFPVNTLIVESW--KSIKD- LSSRRSGDGYPLEVIEPVNSSSLR----- 590	CC	CC
Db	348 K-PFENVIPVLPYQSENWNRCQGGDNITSLGTUNPRTVEFNGYSSPSMRDVSSPP 405	CC	CC
QY	591 -SVSTGSS-RPSKICLVCDEASCHYVTCGCKVFRAVCGHONYCAGRNCTD 648	DR	DR
Db	407 SSSSTATGPPPKCLVCSDEASCHYVLTGCSCKVFRAVCGHONYCAGRNCTD 466	DR	DR
QY	649 KIRKNCPACRLOKQLOAMNIGARKSKKIGKIGIHERSQQQQRPQQPRPPPROSPECT 708	DR	DR
Db	467 KIRRNCPACRYRKCLQAGMNEARAKTK--KIGKI-----QAT 504	DR	DR
QY	709 TYIA-PAKEPSVNTALVPLQSTISRALTFSPVMMLENIBEPIVAGYDSSKPDRENLLS 767	DR	DR
Db	505 TGVQETSSENPAKNTIVP-ATLQ-LTPPLVLSLEPIVAGYDSDVPSDWRMT 561	DR	DR
QY	768 TLNRLAGKONIQVKWAKVLPGLFHNPLPDLTTIYOISWMCLSSFAFLSWRSYKINTSOFL 827	KW	PROSITE; PS00031; NUCLEAR RECEPTOR_1.
Db	562 TLNLMLGGRQVIAVWKAWAKAIPGFRLNLHDQMTLQYSWMFLMAFALGWRSYROASSNLL 621	KW	Receptor; Transcription regulation; DNA-binding; Nuclear protein;
QY	828 YEAQDVLVNE 837	ZINC_FINGER	Zinc-finger; Steroid-binding.
Db	622 CFAPDLLINE 631	DOMAIN	Modulating.
RESULT 9	GCR_SAIBB STANDARD: PRT: 777 AA.	DOMAIN	DNA_BIND
AC	O13186; 15-JUL-1998 (Rel: 36, Created)	FT	42.1 486 NUCLEAR RECEPTOR-TYPE.
DT	15-JUL-1998 (Rel: 36, last sequence update)	FT	ZN_FING 42.1 441 C4-TYPE.
DT	16-OCT-2001 (Rel: 40, last annotation update)	FT	ZN_FING 45.7 481 C4-TYPE.
DE	Glucocorticoid receptor (GR).	FT	DOMAIN 48.7 527 HINGE.
GN	NR3C1 OR GRL.	FT	SEQUENCE 52.8 777 STEROID-BINDING
OS	Saimiri boliviensis boliviensis (Bolivian squirrel monkey).	FT	777 AA; 85611 MW; CE3CD9EBD6A4F3AB CRC64;
OC	Eukaryote; Metazoa; Chordata; Vertebrata; Euteleostomi;	QY	Query Match
OC	Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Saimiri.	Best Local Similarity	19.3%; Score 853; DB 1; Length 777;
OX	NCBI_TaxID:39432;	Matches	30.6%; Pred. No. 3. 5.e-38;
RN	{1} SEQUENCE FROM N.A.	Conservative	103; Mismatches 225; Indels 262; Gaps 32;
RP	TISSUE=Liver;	Indels	129
RC	REMEDINE-97176599; PubMed=9024238;	Gaps	129
RA	Reynolds P.D., Pittler S.J., Scammell J.G.;	ANT	ANT 129
RT	*Cloning and expression of the glucocorticoid receptor from the squirrel monkey (Saimiri boliviensis boliviensis), a glucocorticoid-resistant primate.";	Db	130 NRSTLSSVPE----NPKSSASSVSA-----KEKEFPKTH----- 160
RT	J. Clin. Endocrinol. Metab. 82:465-472(1997).	Db	259 SPLSSPLSSMKSSISSPSPHSCSVKSPVSSPNNTLRSVSSPANI-NNSRCSVSSPNTN 317
RT	THE REGULATION OF EUKARYOTIC GENE EXPRESSION AND AFFECT CELULAR PROLIFERATION AND DIFFERENTIATION IN TARGET TISSUES. BINDS TO THE GRE TARGET SITE.	Db	161 SDVSSEQONLKGQTG-----SNQGVNLKYTADOSTFDIQLDFESSPGKET 208
CC	- !- SUBCELLULAR LOCATION: Nuclear.	QY	318 NRSTLSSPAASTVGSICSPV-NNAFSYTAGTSAGTSAGSSSTDRLWV--SPDQEKAQEVF 374
CC		Db	209 NQSPWKSDLIDENCLLSPLAGEEDSFLLLEGNSN---EDCKPLILPDK----- 254
CC		QY	375 PKTEEVESATISNGVTGOLNIVQYKPEPDGFASCLGGNSKINSDSTSFSVP-IKQESTK 433
CC		Db	255 PKIKD----- 280
CC		DR	EMBL; U87951; AAC51131.1; -.
CC		DR	HSSP; P06536; IGD.
CC		DR	InterPro; IPR00536; Hormone_rec_1g.
CC		DR	InterPro; IPR01628; zf-C4.
CC		DR	InterPro; IPR01409; Glucocorticoid_receptor.
CC		DR	Pfam; PF02155; GCR_1.
CC		DR	Pfam; PF00104; hormone_rec_1.
CC		DR	Pfam; PF00105; zf-C4_1.
CC		DR	PRINTS; PRO0041; STROIDFINGER.
CC		DR	SMART; SM00430; HOLT_1.
CC		DR	SMART; SM0399; ZNF_C4_1.
CC		DR	PROSITE; PS00031; NUCLEAR RECEPTOR_1.
CC		DR	ZINC_FINGER; Steroid-binding.
CC		FT	DOMAIN 1 420 NUCLEAR RECEPTOR-TYPE.
CC		FT	DNA_BIND 42.1 486 NUCLEAR RECEPTOR-TYPE.
CC		FT	ZN_FING 42.1 441 C4-TYPE.
CC		FT	ZN_FING 45.7 481 C4-TYPE.
CC		FT	DOMAIN 48.7 527 HINGE.
CC		FT	SEQUENCE 52.8 777 STEROID-BINDING
CC		FT	777 AA; 85611 MW; CE3CD9EBD6A4F3AB CRC64;





DT 01-NOV-1997 (Rel. 35, Last sequence update) Qy 199 NTMSSVCSPAGINSVSTTASFGSPFVHSPTQGIPPLTCSPNAENRGSRSHSPAHASNVG 258  
 DT 16-OCT-2001 (Rel. 40, Last annotation update) Db 138 NPKSSASS-----SVA-----  
 DE Glucocorticoid receptor (GR).  
 GN NRCAI OR GRL.  
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Saginus.  
 NCBI\_TAXID=9490;  
 RN [1]  
 RP SEQUENCE FROM N.A. MEDLINE=97116699; PubMed=9024238;  
 RX RA Reynolds P.D.; Pittler S.J.; Scamell J.G.;  
 RT "Cloning and expression of the glucocorticoid receptor from the squirrel monkey (*Saimiri boliviensis boliviensis*), a glucocorticoid-resistant primate."  
 RT J. Clin. Endocrinol. Metab. 82:465-472(1997).  
 RL -!- FUNCTION: THE STEROID HORMONES AND THEIR RECEPTORS ARE INVOLVED IN THE REGULATION OF EUKARYOTIC GENE EXPRESSION AND AFFECT CELLULAR PROLIFERATION AND DIFFERENTIATION IN TARGET TISSUES. BINDS TO THE GRE TARGET SITE.  
 CC -!- SUBCELLULAR LOCATION: nuclear.  
 CC -!- DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN, A DNA BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.  
 CC -!- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTOR FAMILY.  
 CC NR3 SUBFAMILY.  
 CC -----  
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 CC -----  
 CC EMBL; U89593; AAC51133.1; -.  
 DR HSSP; P0536; IGD  
 DR InterPro; IPR001409; Glucocorticoid\_receptor.  
 DR InterPro; IPR000536; Hormone\_rec\_lig.  
 DR Pfam; PF02155; zf-C4.  
 DR Pfam; PF00104; hormone\_rec; 1.  
 DR Pfam; PF00105; zf-C4; 1.  
 DR PRINTS; PRO00047; STROIDFINGER.  
 DR SMART; SM0039; Znf\_C4; 1.  
 DR PROSITE; PS00031; NUCLEAR RECEPTOR; 1.  
 KW Receptor; Transcription regulation; DNA-binding; Nuclear protein;  
 KW Zinc-finger; Steroid-binding; NUCLEAR RECEPTOR-TYPE.  
 FT DOMAIN 1 420 MODULATING.  
 FT DNA\_BTMD 421 486 C4-TYPE.  
 FT ZN\_FING 427 481 C4-TYPE.  
 FT DOMAIN 487 527 HINGE.  
 FT DOMAIN 528 777 STEROID-BINDING.  
 SQ SEQUENCE 777 AA; 85593 MW; E4FD24ABC5FD958 CRC64;

Query Match 19.1%; Score 845; DB 1; Length 777; Best Local Similarity 30.5%; Pseq: 9.3e-38; Pseq No. 103; Mismatches 259; Conservative 227; Indels 260; Gaps 32; Matches 259; Conservative 227; Indels 260; Gaps 32;

Qy 28 RSSLGPRTEDDENYM-EIVWSCVSGALPNNSTCGSSKEREQELPCLQDNNRPGILT 85 ID GCR\_MOUSE STANDARD; PRT: 783 AA.  
 ID GCR\_MOUSE  
 AC P06537; 061628; Q61629;  
 DT 01-JAN-1998 (Rel. 06, Created)  
 DT 01-JAN-1998 (Rel. 06, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Glucocorticoid receptor (GR).  
 GN NR3C1 OR GRL OR GR.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OC Mammalia; Buterilia; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OC NCBI\_TAXID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A. MEDLINE=87053816; PubMed=3780669;  
 RX -----  
 RA Danielsen M., Northrop J.P., Ringold G.M.;  
 RA The mouse glucocorticoid receptor: mapping of functional domains by cloning, sequencing and expression of wild-type and mutant receptor proteins.".  
 RL EMBO J. 5:2513-2522(1986).  
 RN [2]  
 RP SEQUENCE OF 1-155 FROM N.A. MEDLINE=89098404; PubMed=291477;



- RT a study of allele frequencies in inbred and wild rat populations  
 RT and of the steroid-binding properties of their polypeptides in  
 vitro."; to the EMBL/genBank/DDBJ databases.
- RN [3] SEQUENCE OF 1-515 FROM N.A.  
 RL STRAIN="SPRAGUE-DAWLEY"; TISSUE="prostate";  
 RC MEDLINE="88067783"; PubMed=3684608;  
 RA Chang C., Kokontis J., Chang C.T., Liao S.;  
 RT "cloning and sequence analysis of the rat ventral prostate  
 glucocorticoid receptor cDNA";  
 RT Nucleic Acids Res. 15:9603-9603(1987).  
 RL [4] Nucleic Acids Res. 15:9603-9603(1987).  
 RP MUTAGENESIS OF ZINC FINGER.  
 RX MEDLINE="89052664"; PubMed=3191912;  
 RA Severini Y., Wieland S., Schaffner W., Rusconi S.;  
 RT "Metal binding 'finger' structures in the glucocorticoid receptor  
 defined by site-directed mutagenesis.";  
 RL EMBO J. 7:2503-2508(1988).  
 RN [5] Nucleic Acids Res. 21:2014-2014(1993).  
 RP MUTAGENESIS OF ZINC FINGER.  
 RX MEDLINE="93195921"; PubMed=4450530;  
 RA Zandi E., Galli I., Doebbeling U., Rusconi S.;  
 RT Zinc finger mutations that alter domain interactions in the  
 glucocorticoid receptor.";  
 RL J. Mol. Biol. 230:124-136(1993).  
 RN [6] REVIEW ON MUTAGENESIS.  
 RX MEDLINE="94249031"; PubMed=8191545;  
 RA Lanz R.B., Hug M., Gola M., Tallone T., Wieland S., Rusconi S.;  
 RT "Active-, interactive-, and inactive steroid receptor mutants.";  
 RL Steroids 59:148-152(1994).  
 RN [7] X-RAY CRYSTALLOGRAPHY OF 440-525.  
 RX MEDLINE="91326070"; PubMed=1865905;  
 RA Luisi B.F., Xu W.X., Otwowski Z., Freedman I.P., Yamamoto K.R.,  
 RA Stigler P.B.;  
 RT "Crystallographic analysis of the interaction of the glucocorticoid  
 receptor with DNA";  
 RL Nature 352:497-505(1991).  
 RN [8] STRUCTURE BY NMR OF 440-510.  
 RX MEDLINE="90319784"; PubMed=2115209;  
 RA Haerd T., Keillenbach E., Boelens R., Maler B.A., Dahlman K.,  
 RA Freedman L.P., Carlstedt-Duke J., Yamamoto K.R., Gustafsson J.-A.,  
 RA Kaptein R.;  
 RT "Solution structure of the glucocorticoid receptor DNA-binding  
 domain";  
 RL Science 249:157-160(1990).  
 RN [9] STRUCTURE BY NMR OF 440-525.  
 RX MEDLINE="92089066"; PubMed=1751485;  
 RA Vemrowski M.L., Keillenbach E., Boelens R., van der Marel A.,  
 RA van Boom J.H., Maler B.A., Yamamoto K.R., Kaptein R.;  
 RT "1H NMR studies of DNA recognition by the glucocorticoid receptor:  
 complex of the DNA binding domain with a half-site response  
 element";  
 RL Bichemistry 30:11620-11624(1991).  
 RN [10] STRUCTURE BY NMR OF 440-525.  
 RX MEDLINE="92038072"; PubMed=1936288;  
 RA Keillenbach E., Maler B.A., Yamamoto K.R., Boelens R., Kaptein R.;  
 RT "Identification of the metal coordinating residues in the DNA binding  
 domain of the glucocorticoid receptor by 113cd-1H heteronuclear NMR  
 spectroscopy";  
 RT FEBS Lett. 291:367-370(1991).  
 RL [11] STRUCTURE BY NMR OF 439-510.  
 RX MEDLINE="4079877"; PubMed=825-681;  
 RA Baumann H., Paulsen K., Kovacs H., Berglund H., Wright A.P.H.,  
 RA Gustafsson J.-A., Haerd T.;  
 RT "Refined solution structure of the glucocorticoid receptor DNA-binding  
 domain";

- RL Biochemistry 32:13463-13471(1993).  
 RN [12] STRUCTURE IN POLY-GIN REGION.  
 RP VARIANTS IN POLY-GIN REGION.  
 RX MEDLINE="93261843"; PubMed=8493115;  
 RA Gearing K.L., Gustafsson J.-A., Okret S.;  
 RT "Heterogeneity in the polyglutamine tract of the glucocorticoid  
 receptor from different rat strains";  
 RL Nucleic Acids Res. 21:2014-2014(1993).  
 CC -!- FUNCTION: THE STEROID HORMONES AND THEIR RECEPTORS ARE INVOLVED IN  
 THE REGULATION OF EUKARYOTIC GENE EXPRESSION AND AFFECT CELLULAR  
 PROLIFERATION AND DIFFERENTIATION IN TARGET TISSUES. BINDS TO THE  
 CC GRE TARGET SITE.  
 CC -!- SUBCELLULAR LOCATION: Nuclear.  
 CC -!- DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN,  
 CC A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.  
 CC -!- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.  
 CC NR3 SUBFAMILY.  
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 CC -----  
 DR EMBL; M1053; AAA41203.; --.  
 DR EMBL; Y00489; CAA68545.; --.  
 DR EMBL; X12264; CRA72938.; --.  
 DR EMBL; X69666; ; NOT\_ANNOTATED\_CDS.  
 DR EMBL; X69668; ; NOT\_ANNOTATED\_CDS.  
 DR EMBL; X69669; ; NOT\_ANNOTATED\_CDS.  
 DR EMBL; X69670; ; NOT\_ANNOTATED\_CDS.  
 DR PIR; A24194; QRTG.  
 DR PDB; 1GDC; 22-JUN-94.  
 DR PDB; 2GDA; 22-JUN-94.  
 DR PDB; 1RGD; 14-FEB-95.  
 DR TRANSFAC; T00333; --.  
 DR InterPro; IPR01409; Glucocorticoid\_receptor.  
 DR InterPro; IPR00536; Hormone\_rec\_lig.  
 DR PRINTS; PRO0047; STROIDFINGER.  
 DR SMART; SM0430; HOLI\_1.  
 DR SMART; SM0399; Znf\_C4; 1.  
 KW PROSITE; PS00031; NUCLEAR RECEPTOR; 1.  
 KW Receptor; Transcription regulation; DNA-binding; Nuclear protein;  
 KW Zinc-finger; Steroid-binding; Polymorphism; 3D-structure.  
 FT DOMAIN\_1 DOMAIN  
 FT DOMAIN\_BIND 440 505 NUCLEAR RECEPTOR-TYPE.  
 FT DOMAIN\_BIND 440 505 NUCLEAR RECEPTOR-TYPE.  
 FT ZN\_FING 440 460 C4-TYPE.  
 FT ZN\_FING 476 500 C4-TYPE.  
 FT DOMAIN 506 795 STEROID-BINDING.  
 FT DOMAIN 75 97 POLY-GIN.  
 FT VARIANT 83 96 MISSING (IN SPRAGUE-DAWLEY).  
 FT VARIANT 226 226 S -> G.  
 FT VARIANT 260 260 N -> D.  
 FT VARIANT 260 260 D -> G (IN REF. 1).  
 FT CONFLICT 98 98 S -> T (IN REF. 3).  
 FT CONFLICT 345 345 L -> P (IN REF. 2).  
 FT STRAND 600 600 HELIX 458 469  
 FT STRAND 600 600 TURN 486 487  
 FT STRAND 439 439 HELIX 488 490  
 RT TURN 491 491



QY	86	SDIK---TELESKELSATVAESMGLYM---DSVRDADYSFQQNOOGSMSPAKIYQNE	138
Db	124	ESTI-----	ANL 129
Qy	199	NMTSSVCSPAGINSVSSTASAFGSFPVHSPTQGTPILRCSPNAENGRSRSHSPAHASNVG	258
Db	130	NRSTSVEP---NPKSSASSSVSAP-----KEKERPKH-----	160
Qy	259	SPLSPPLSSMKSSISPPSCHCSVSKSPVSPPNNTLRSVSSPANI-NNSRSRVSSPSNTN	317
Db	161	SDVSSQSNKJGQTG-----TNGNRYKLYTADQSTFDLQDFESSGSPKET	208
Qy	318	NRSTLSPLSPAATVGSCSICPV--NNASRSTYASGTSGSSTLRDVVP--SPDTQERGAQEVPF	374
Db	209	NQSPWRSPLDLIDENGLLSPLAGERSDESFLEGENSN----EDCKPLLPDTR-----	254
Qy	375	PKTEEVESATISNGVTGQLNIVQYIKPEPDGAFSSCLGGNSKINSDSSFSVP-IKQESTK	433
Db	255	I -----PKKD-----	280
Qy	434	HSCSGTSFKGNPTVNBPFPMEDGSYFSFMDRDYVSLSGLJPGVPGFGCEGSGFFVG	493
Db	281	-----EDFELC-----TPGV-----I	292
Qy	494	KOEPDPGSYYPEBEAIPSSAIVG-----VNSGGOSPHYRGAQTSIUSRSARDQ	542
Db	293	KQE-KISTIVYCQASFPGGANLTIGNKAISLIGHVSTSGGOMYHD-----NTASLSQO-QDO	347
Qy	543	SIQHLLSSFPVNTLVEW-----KSHD-----SSRRSDGYPLEYIPENVSSTL-----	590
Db	348	K-PFIVNTPITPGVSENNRQCGSDNLN-----SLGTLNFPGTVFSGNGYSSPSMRPDVSSPP	406
Qy	591	-SVSTGSS-RSKICJCGDASGCHGYYTGCSSOKYEVKRAVGQHNYLCAGRNDCTID	648
Db	407	SSSSTATTPPPPKLCLVCSDEASGCHGYYTGCSSOKYEVKRAVGQHNYLCAGRNDCTID	466
Qy	649	KIRRNKGCPACRLQKCIQAGMNIGARKSKKKLGKLGTHEEQPQQOPPPPPQPSPEGT	708
Db	467	KIRRNKGCPACRLQKCIQAGMNIGARKSKKKLGKLGTHEEQPQQOPPPPPQPSPEGT	505
Qy	709	TYTA-PAKEPSVNTALYPOLOSTISRALTPSPVMVLENIEPIVAGYDSSKPDTAENLIS	767
Db	506	TGVSQETSENPNPANTIVP---ATLQO-LTPLUVLLEVIEFVLYAGYDSTVPSDSTWRINT	562
Qy	768	TUURLAGKQMITQVKWAKVLRDFPKNPLEDOIITLTOYSWMCILSSFTALSWSYKTNQFL	827
Db	563	TLMNLGGRQVIAAVKWAQKAIPOFRNLHLDOMTLOQYSWMLFMAFLGNNSYRQASSNL	622
Qy	828	YFAPDVLVNE 837	
Db	623	CFAIDLINNE 632	

Search completed: September 13, 2002, 10:21:51  
Job time: 290 sec

genCore version 4.5  
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## OM protein - protein search, using sw model

Run on: September 13, 2002, 10:16:26 ; Search time 37.65 Seconds  
(without alignments)

3882.622 Million cell updates/sec

Title: US\_09-695\_293\_42

Perfect score: 4422

Sequence: 1 METKGHSLPGLDMERRWG . . . . . FLYFAPDVLVNELLARVREG 845

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 10%

Listing first 45 summaries

Database : SPREMBL\_19;\*

1: sp\_rembl\_19;\*

2: sp\_bacteria;\*

3: sp\_fungi;\*

4: sp\_human;\*

5: sp\_invertebrate;\*

6: sp\_mammal;\*

7: sp\_minc;\*

8: sp\_organelle;\*

9: sp\_phage;\*

10: sp\_plant;\*

11: sp\_rabbit;\*

12: sp\_virus;\*

13: sp\_vertebrate;\*

14: sp\_unclassified;\*

15: sp\_virus;\*

16: sp\_bacteriapl;\*

17: sp\_archaea;\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

# Query Match Length DB ID Description

Result No.	Score	Match	Length	DB	ID	Description
1	4262	96.4	982	6	Q9N0W8	Ogn0w8 saimiri sci
2	3515	79.5	706	4	Q86K09	096kq9 homo sapien
3	807.5	18.3	732	13	Q9DD09	Q9dd09 xenopus lae
4	787.5	17.8	438	13	Q9ZB07	Q90zm7 petromyzon
5	779.5	17.6	939	6	Q9GLW0	Q9glw0 canis famili
6	764.5	17.3	583	13	Q9DEV4	Q9dev4 xenopus lae
7	756.5	17.1	710	13	Q9IBD5	Q9ibd5 anquilla ja
8	754	17.1	853	13	Q93245	Q93245 oncophrychu
9	748.5	16.9	896	6	Q9KL7	Q9kl7 sus scrofa
10	747	16.9	360	13	Q42274	Q42274 crocodylus
11	745.5	16.9	359	13	Q9IAC6	Q9iac6 oncorhynchus
12	741.5	16.8	895	6	Q9GK9	Q9gk9 sus scrofa
13	739	16.7	790	13	P70048	P70048 xenopus lae
14	729.5	16.5	906	4	Q9UN21	Q9un21 homo sapien
15	729	16.4	848	13	Q9YGV9	Q9ygv9 anguilla ja
16	724	16.4	797	13	Q9Pwg5	Q9pwg5 anguilla ja

17	719.5	16.3	769	13	Q93497	pagrus major
18	715.5	16.2	401	13	Q90ZM6	090zm6 petromyzon
19	714.5	16.2	563	13	Q9DDJ4	09ddj4 halichoeres
20	709.5	16.0	854	13	Q93244	093244 oncorhynchus
21	708	16.0	730	4	Q13771	homo sapien
22	669.5	15.1	303	6	Q97684	097684 ovis aries
23	644.5	14.6	344	13	Q91445	091445 serinus can
24	638.5	14.4	692	13	Q9W6F4	09w6f4 haplochromis
25	634.5	14.3	348	13	Q91425	091425 ctenoides
26	602.5	13.6	284	13	Q9Y000	090y00 petromyzon
27	539.5	12.2	232	13	Q9TA30	09ta30 anolis caro
28	529	12.0	258	6	Q9BU77	Q9bu77 ovis aries
29	495.5	11.2	298	6	Q28547	Q28547 ovis aries
30	486	11.0	200	13	Q918F5	0918f5 pimphales
31	457.5	10.3	164	13	Q90ZC2	Q90zc2 calotes ver
32	449.5	10.2	166	13	Q91698	091698 xenopus lae
33	445.5	10.1	554	13	Q90ZM8	090zm8 petromyzon
34	434	9.8	553	13	Q90WS8	Q90ws8 brachydanio
35	429.5	9.7	431	6	Q95LJ3	Q95lj3 ovis aries
36	422.5	9.6	153	11	Q923G6	Q923g6 mesocricetus
37	422	9.5	499	6	Q95MF0	Q95mf0 macaca arct
38	422	9.5	526	6	Q9Bdw5	Q9bdw5 sus scrofa
39	420	9.5	553	13	Q9BSM7	Q9bsm7 brachydanio
40	414	9.4	569	13	Q90SM9	Q90sm9 brachydanio
41	412	9.3	564	13	Q90WV1	Q90wv1 carassius a
42	410.5	9.3	620	13	Q90WH6	Q90wh6 clarilas gar
43	406.5	9.2	250	6	Q95JC0	Q95jc0 canis familiaris
44	401.5	9.1	592	13	Q90WS9	Q90ws9 brachydanio
45	400.5	9.1	486	6	Q95ME9	Q95me9 callithrix

## ALIGNMENTS

RESULT	1	Q9NW8	PRELIMINARY;	PRM;	982 AA.
ID	Q9NW8;				
AC	Q9NW8;				
DT	01-OCT-2000	(TREMBLrel. 15, Created)			
DT	01-OCT-2000	(TREMBLrel. 15, Last sequence update)			
DT	01-DEC-2001	(TREMBLrel. 19, Last annotation update)			
DE	MENRAUCOCORTICOID RECEPTOR.				
OS	Saimiri sciureus (Common squirrel monkey).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
CC	Mammalia; Eutheria; Primates; Platyrhini; Cebidae; Cebinae; Saimiri.				
OX	NCBI_TaxID=9521;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RA	Patel P.D.;				
RT	"squirrel monkey Mineralocorticoid Receptor cDNA";				
RL	Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.				
CC	-!- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.				
DR	EMBL; AF245224; RAP63382.1; -.				
DR	HSSP; P06536; 1RQD.				
DR	Inter-Pro; IPR00536; Hormone_rec_lig.				
DR	InterPro; IPR001723; Strdiormone_receptor.				
DR	PFam; PF00104; zf-C4.				
DR	PRINTS; PR00388; STRDIORMONER.				
DR	SMART; SM00430; HOLL; 1.				
DR	PROSITE; PS00399; Znf_C4.				
DR	PROSITE; PS00331; NUCLEAR_RECEPTOR; 1.				
KW	DNA-binding; Nuclear protein; Receptor; Transcription regulation;				
KW	Zinc-finger.				
SO	SEQUENCE 982 AA; 107084 MW; E90C37E3302BC046 CRC64;				

Query	Match	Length	DB	ID	Description
Query	Match	Length	DB	ID	Description
Best Local Similarity	97.7%	Score	4262;	DB 6;	Length 982;
Matches	818;	Conservative	3;	Mismatches	14;
Indels	2;	Gaps	2;		

QY	1 METKGYHSLPEGLIDMERGQVSQAVERSSLGPTERTDENNYMEIVNVSCVSGAIPNNT	RX	MEDLINE=21410115; PubMed=11518808;
Db	1 METKGYHSLPEGLIDMERGQVSQAVERSSLGPTERTDENNYMEIVNVSCVSGAIPNNT	RA	Zennaro M.C., Souque A., Viengchareun S., Poisson E., Lambre M.;
QY	61 QGSSEKEOELLPCQLQDNRPGITSDIKTELESKELSATVAESMGLYMDSVRADSYE	RT	"A new human MR splice variant is a ligand-independent transactivator
Db	61 QGSSEKEOELLPCQLQDNRPGITSDIKTELESKELSATVAESMGLYMDSVRADSYE	modulating corticosteroid action.";	
QY	121 QQNQGMSMSPAKTYVNEOLVKFYKGNGRPSTLSCVNPLRSRPMDSGSSVNGGYMRAI	RL	Mol. Endocrinol. 15:1586-1598(2001).
Db	120 QQNQGMSMSPAKTYVNEOLVKFYKGNGRPSTLSCVNPLRSRPMDSGSSVNGGYMRAI	DR	EMBL: J315514; CAC67405.1; -;
QY	181 VKSPIMCHERSPSVCSPLNMSSVCPAGINSVSSTASFGSPVHSPIQTGPTLCSPN	KW	SEQUENCE: 706 AA: 75066 MW: 03CF63D0ACEE981C CRC64;
Db	180 VKSPIMCHERSPSVCSPLNMSSVCPAGINSVSSTASFGSPVHSPIQTGPTLCSPN	Receptor:	
QY	241 AENRORSRSHPAHASVGSPLSLSSPSSMSSISPPSPHSVSVSPVSPNNTLRSSVP	Query Match	79.5%; Score 3515; DB 4; length 706;
Db	240 VENGRSRSHPAHASVGSPLSLSSPSSMSSISPPSPHSVSVSPVSPNNTLRSSVP	Best Local Similarity	99.4%; Pred. No. 2.4e-229;
QY	301 ANINNSRCSPSSPNTRNRLSPLSPAATVGSTICSPVNNAFSTYASGTAGSSTLRDV	Matches	2; Mismatches 0; Gaps 0;
Db	300 ANINNSRCSPSSPNTRNRLSPLSPAATVGSTICSPVNNAFSTYASGTAGSSTLRDV	Indels	0;
QY	361 SPDTOKGAGQEVPKTTEEVESETASNGVQLNIVOTYKPEPDGFSSCGGNSKIND	Db	1 QGSSEKEOELLPCQLQDNRPGITSDIKTELESKELSATVAESMGLYMDSVRADSYE
Db	360 SPDTOKGAGQEVPKTTEEVESETASNGVQLNIVOTYKPEPDGFSSCGGNSKIND	QY	61 QGSSEKEOELLPCQLQDNRPGITSDIKTELESKELSATVAESMGLYMDSVRADSYE
QY	421 SSFSVPIKOSKTHKSCSGTSFKGNPVTNPPEMDGSYSFMDKDYSLGILGPVPGF	Db	61 QGSSEKEOELLPCQLQDNRPGITSDIKTELESKELSATVAESMGLYMDSVRADSYE
Db	420 SSFSVPIKOSKTHKSCSGTSFKGNPVTNPPEMDGSYSFMDKDYSLGILGPVPGF	QY	121 QQNQGMSMSPAKTYVNEOLVKFYKGNGRPSTLSCVNPLRSRPMDSGSSVNGGYMRAI
QY	481 DGCEGSGFPVKGKQEPDDGSYYPEASIPSAVINGNSGQSFHYRIGAGTISLSAR	Db	121 QQNQGMSMSPAKTYVNEOLVKFYKGNGRPSTLSCVNPLRSRPMDSGSSVNGGYMRAI
Db	480 DGCEGSGFPVKGKQEPDDGSYYPEASIPSAVINGNSGQSFHYRIGAGTISLSAR	QY	181 VKSPIMCHERSPSVCSPLNMSSVCPAGINSVSSTASFGSPVHSPIQTGPTLCSPN
QY	541 DOSFOHLSFPVNTLVESWKSHGDLSRSDGYPLEYIPENVSSTLRSSVGSRRPS	Db	181 VKSPIMCHERSPSVCSPLNMSSVCPAGINSVSSTASFGSPVHSPIQTGPTLCSPN
Db	540 DOSFOHLSFPVNTLVESWKSHGDLSRSDGYPLEYIPENVSSTLRSSVGSRRPS	QY	121 QQNQGMSMSPAKTYVNEOLVKFYKGNGRPSTLSCVNPLRSRPMDSGSSVNGGYMRAI
QY	601 KICLVCGDEASGCHGCVTCGCKVFKRAVEQEGQHNYLCAGRNDCIDKIRRNCPACRL	Db	121 QQNQGMSMSPAKTYVNEOLVKFYKGNGRPSTLSCVNPLRSRPMDSGSSVNGGYMRAI
Db	600 KICLVCGDEASGCHGCVTCGCKVFKRAVEQEGQHNYLCAGRNDCIDKIRRNCPACRL	QY	181 VKSPIMCHERSPSVCSPLNMSSVCPAGINSVSSTASFGSPVHSPIQTGPTLCSPN
QY	661 OKCLOAGMLGARKSKKGKLGKLGTHEQPOQOPPPPPPPQSPERGTYTAPAKPSVN	Db	181 VKSPIMCHERSPSVCSPLNMSSVCPAGINSVSSTASFGSPVHSPIQTGPTLCSPN
Db	660 OKCLOAGMLGARKSKKGKLGKLGTHEQPOQOPPPPPQSPERGTYTAPAKPSVN	QY	121 QQNQGMSMSPAKTYVNEOLVKFYKGNGRPSTLSCVNPLRSRPMDSGSSVNGGYMRAI
QY	721 TALYVPLSTISRALTPSPVMVLENIEPEIIVAGYDSSKPDTAENLSTLNRLAGKOMIOV	Db	121 QQNQGMSMSPAKTYVNEOLVKFYKGNGRPSTLSCVNPLRSRPMDSGSSVNGGYMRAI
Db	719 TALYVPLSTISRALTPSPVMVLENIEPEIIVAGYDSSKPDTAENLSTLNRLAGKOMIOV	QY	181 VKSPIMCHERSPSVCSPLNMSSVCPAGINSVSSTASFGSPVHSPIQTGPTLCSPN
QY	781 VKKAVKVLGFKNUPLEDQITLIQYSWMLCLSLTSLMSWPSYKHNSQFLYFADLVE	Db	181 VKSPIMCHERSPSVCSPLNMSSVCPAGINSVSSTASFGSPVHSPIQTGPTLCSPN
Db	779 VKKAVKVLGFKNUPLEDQITLIQYSWMLCLSLTSLMSWPSYKHNSQFLYFADLVE	QY	121 QQNQGMSMSPAKTYVNEOLVKFYKGNGRPSTLSCVNPLRSRPMDSGSSVNGGYMRAI
RESULT	2	Db	121 QQNQGMSMSPAKTYVNEOLVKFYKGNGRPSTLSCVNPLRSRPMDSGSSVNGGYMRAI
Q96KQ9	PRELIMINARY; PRT: 706 AA.	Q96KQ9	121 QQNQGMSMSPAKTYVNEOLVKFYKGNGRPSTLSCVNPLRSRPMDSGSSVNGGYMRAI
AC		Q96KQ9	121 QQNQGMSMSPAKTYVNEOLVKFYKGNGRPSTLSCVNPLRSRPMDSGSSVNGGYMRAI
DT	01-DEC-2001 (TREMBlrel. 19, Created)	Q96KQ9	121 QQNQGMSMSPAKTYVNEOLVKFYKGNGRPSTLSCVNPLRSRPMDSGSSVNGGYMRAI
DT	01-DEC-2001 (TREMBlrel. 19, Last sequence update)	Q96KQ9	121 QQNQGMSMSPAKTYVNEOLVKFYKGNGRPSTLSCVNPLRSRPMDSGSSVNGGYMRAI
DE	MINERALOGORTICOID RECEPTOR DELTA.	Q96KQ9	121 QQNQGMSMSPAKTYVNEOLVKFYKGNGRPSTLSCVNPLRSRPMDSGSSVNGGYMRAI
GN	MR.	Q96KQ9	121 QQNQGMSMSPAKTYVNEOLVKFYKGNGRPSTLSCVNPLRSRPMDSGSSVNGGYMRAI
OS	Homo sapiens (Human).	Q96KQ9	121 QQNQGMSMSPAKTYVNEOLVKFYKGNGRPSTLSCVNPLRSRPMDSGSSVNGGYMRAI
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;	Q96KQ9	121 QQNQGMSMSPAKTYVNEOLVKFYKGNGRPSTLSCVNPLRSRPMDSGSSVNGGYMRAI
NCBI_TaxID	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Q96KQ9	121 QQNQGMSMSPAKTYVNEOLVKFYKGNGRPSTLSCVNPLRSRPMDSGSSVNGGYMRAI
RN	[1] SEQUENCE FROM N.A.	Q96KQ9	121 QQNQGMSMSPAKTYVNEOLVKFYKGNGRPSTLSCVNPLRSRPMDSGSSVNGGYMRAI
RP		Q96KQ9	121 QQNQGMSMSPAKTYVNEOLVKFYKGNGRPSTLSCVNPLRSRPMDSGSSVNGGYMRAI



AC	09GLW0;	QY	623 CKVFRKRAVEQHNYICAGRNDC1TEKIRRNKCACRQLCQLQAGMNLGARKSKKGKIK
DT	01-MAR-2001 (TREMBLrel. 16, Last sequence update)	Db	593 CKVFPRKRAMEQGQHNTLCAGRDCTVKRKNCPACRLRKCCQAGMVLGRKFKKFNVK 652
DT	01-MAR-2001 (TREMBLrel. 16, Last sequence update)	QY	683 GIHE-BQPOQQOQPPIPQPSERGTTYAKAPEFSVNTVQLISTISRALTPSPWV 741
DE	PROGESTERONE RECEPTOR.	Db	653 VMRLDVALRQPVGIPNNEQSALSRRISF----SSPDQIQLPPL-----INL 696
GN	Canis familiaris (Dog).	Db	593 CKVFPRKRAMEQGQHNTLCAGRDCTVKRKNCPACRLRKCCQAGMVLGRKFKKFNVK 652
OS	"Molecular cloning and cellular localization of the canine progesterone receptor."; submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.	QY	683 GIHE-BQPOQQOQPPIPQPSERGTTYAKAPEFSVNTVQLISTISRALTPSPWV 741
RA	SEQUENCE FROM N.A. Lantinga-van Leeuwen I.S., van Garderen E., Mol J.A.; RT Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Butherea; Carnivora; Fissipedia; Canidae; Canis.	Db	653 VMRLDVALRQPVGIPNNEQSALSRRISF----SSPDQIQLPPL-----INL 696
OX	[1] NCBI_TAXID=9615;	QY	742 LENIEEIVVAGYGDSSKDPTAENLLSTLNRLAGKOMIQVWAKWVLPGKNUPLDEDQITL 801
RN	[1]	Db	697 LMSIEPDVIVAGHDNKPDISSSLTSNLGEROLLSVVKWSLPGERNLHTDDQITL 756
CC	-!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).	QY	802 IQYSWMLSSPALSWSWYKHNQSOFYFAPDVLVENLLARYE 844
DR	-!- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.	Db	757 IQYSWMLMVFGLGWWSYKHVGOMLYFAPDLIN--QRME 797
DR	EMBL; AF177470; AAG09282.1; -.	RN	[1]
DR	HSSP; P06401; 1x28.	RESULT	6
DR	InterPro; IPR00536; Hormone_rec_lig.	Q9DEV4	PRELIMINARY;
DR	InterPro; IPR00128; Progesterone_receptor.	ID	Q9DEV4
DR	InterPro; IPR01723; Strd hormone receptor.	AC	Q9DEV4
DR	InterPro; IPR01628; zf-C4.	DT	01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DR	Pfam; PF00104; Hormone_rec; 1.	DT	01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DR	Pfam; PF02161; Prog_receptor; 1.	DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DR	Pfam; PF00105; zf-C4; 1.	DE	PROGESTERONE RECEPTOR PR.
DR	PRINTS; PRO00398; STRD HORMONER.	OS	Xenopus laevis (African clawed frog).
DR	PRINTS; PRO0047; STROIDFINGER.	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
DR	SMART; SM00430; HOLL-1.	OC	Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
DR	SMART; SM00431; NUCLEAR RECEPTOR; 1.	OC	Xenopoda; Xenopus.
DR	PROSITE; PS00031; NUCLEAR RECEPTOR; 1.	OX	NCBI_TAXID=6355;
KW	Zinc-finger; Nuclear protein; Receptor; Transcription regulation;	RN	[1]
SEQUENCE	939 AA; 98417 MW; 14AB8E535A64FF239 CRC64;	RP	SEQUENCE FROM N.A.
RX	MEDLINE=20524048; Pubmed=11050156;	RX	Bayaa M., Booth R.A., Sheng Y., Liu X.J.;
RA	"The classical progestrone receptor mediates Xenopus oocyte	RT	maturation through a nongenomic mechanism";
RT	maturation through a nongenomic mechanism";	RT	Proc. Natl. Acad. Sci. U.S.A. 97:12607-12612(2000).
RL	-!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).	CC	-!- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
CC	-!- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTOR.	DR	EMBL; AT001198; AAG01366.1; -.
DR	InterPro; IPR00536; IRGD.	DR	InterPro; IPR00536; Hormone_rec_lig.
DR	InterPro; IPR00128; Progesterone_receptor.	DR	InterPro; IPR01123; Strd hormone receptor.
DR	InterPro; IPR01628; zf-C4.	DR	InterPro; IPR01628; zf-C4.
DR	Pfam; PF00104; Hormone_rec; 1.	DR	Pfam; PF02161; Prog_receptor; 1.
DR	Pfam; PF00105; zf-C4; 1.	DR	PRINTS; PRO00105; zf-C4; 1.
DR	PRINTS; PRO00198; STRD HORMONER.	DR	PRINTS; PRO0047; STROIDFINGER.
DR	SMART; SM00430; HOLL-1.	DR	SMART; SM00431; NUCLEAR RECEPTOR; 1.
DR	PROSITE; PS00031; NUCLEAR RECEPTOR; 1.	DR	Zinc-finger; Nuclear protein; Receptor; Transcription regulation;
KW	Zinc-finger; Nuclear protein; Receptor; Transcription regulation;	SQ	SEQUENCE 583 AA; 66156 MW; 638D3572C32BD86C CRC64;
SEQUENCE	583 AA; 66156 MW; 638D3572C32BD86C CRC64;	Q9DEV4	PRELIMINARY;
Query	Match 17.3%; Score 764.5; DB 13; Length 583;	QY	623 CKVFRKRAVEQHNYICAGRNDC1TEKIRRNKCACRQLCQLQAGMNLGARKSKKGKIK
Best	Local Similarity 37.9%; Pred. No. 1.6e-43;	Db	593 CKVFPRKRAMEQGQHNTLCAGRDCTVKRKNCPACRLRKCCQAGMVLGRKFKKFNVK 652
Matches	56; Mismatches 134; Indels 113; Gaps 16;	QY	683 GIHE-BQPOQQOQPPIPQPSERGTTYAKAPEFSVNTVQLISTISRALTPSPWV 741
QY	361 SPDRDKGAEVVPKTEEVESATSGNGVQLNTWVQVKE-PDGAFSSCLGGNSKIN 418	Db	653 VMRLDVALRQPVGIPNNEQSALSRRISF----SSPDQIQLPPL-----INL 696
QY	51 SPPDSQ---TSVPENLQPNVKOIS-----YFNPFEIQD-----PRK 85	Db	593 CKVFPRKRAMEQGQHNTLCAGRDCTVKRKNCPACRLRKCCQAGMVLGRKFKKFNVK 652
QY	419 SDSS---FSVPVIKESTHKSCSGTSFKGNPTVNFFPMGSITFSFMDDKYSSLGIG 474	QY	742 LENIEEIVVAGYGDSSKDPTAENLLSTLNRLAGKOMIQVWAKWVLPGKNUPLDEDQITL 801
Db	86 KDSSTVSLYKAAK ESTLCQDYSSPRNPSTPPDSDFLYK-NEDYDFCRIS--- 139	Db	697 LMSIEPDVIVAGHDNKPDISSSLTSNLGEROLLSVVKWSLPGERNLHTDDQITL 756
QY	475 PPVPFDGNGEGSGFPVGIKOPDGSYYPEASIFSSATGVNNSGGQSFHYRIGAQ-T 532	QY	802 IQYSWMLSSPALSWSWYKHNQSOFYFAPDVLVENLLARYE 844
Db	140 -----HGN-----TNEDSGCILPSTS-----AQTYQPLSINGHRY 170	Db	757 IQYSWMLMVFGLGWWSYKHVGOMLYFAPDLIN--QRME 797

QY	533 ISLSRSARDOSRFOHLSFPVNPNTLVEWSWKSHGDLSSRRSDGYPVLEYIPENVSSTLRSV 592
Db	171 VTPOPTPKETEYLPOIQILPYVITYI-----RSDGDE-RGIPFSF----- 208
QY	533 STGSSRSPKICJUCGDEASGCCWVWCGSCWKFKRAVEGONYLCAGRNCIDIRR 652
Db	209 ---EMLPKICLICLGDEASGCCWVWCGSCWKFKRAVEGONYLCAGRNCIDIRR 265
QY	653 KNGPACRLQKLCAGMNIGARKSKKLKGIIHEEQPOQQQPQSPBEGTYIA 712
Db	266 KNGPSCRURKCCAGMILGGRKFRKRKTRRERIDWVQSP----- 308
QY	713 PAKEPSVNTALYVQLSITR--ALTSPVPMLENIREPIVYAGYDSSKPDTAENLSTL 769
Db	309 PTLSLECOQILIRRISNSAQETQFTPELQIQSIEPEVWVAGYDNTQPEPSALLSL 368
QY	770 NRAGKQMIQVWVKAWKVLPKGFLNPKLQDQITILOYSWCMSCLSSFLSRSYKUNINSQFLY 829
Db	369 NOLCEROLIVCVVWKSLSLPGFRNLHIDQITILOYSWMSLMVFALGWRSYOHSGQMLYF 428
QY	830 APPLVNFN 837
Db	429 APPLLINE 436
RESULT	7
Q9IBDS	PRELIMINARY; PR#: 710 AA.
ID	Q9IBDS
AC	01-OCT-2000 (TREMBlrel. 15, Created)
DT	01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT	01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE	PROGESTERONE RECEPTOR.
GN	PR.
OS	Anguilla japonica (Japanese eel).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
OC	Actinopterygii; Neopterygii; Teleostei; Anguilliformes; Anguilloidei;
OC	NBII_TaxID=7937;
RN	[1]
RC	SEQUENCE FROM N.A.
RC	TISSUE-TESTS;
RX	MEDLINE-20088790; PubMed=10620698;
RA	Todo T., Ikeuchi T., Kobayashi T., Kajiwara-Kobayashi H., Suzuki K.,
RA	Yoshikuni M., Yamauchi K., Nagahama Y.; Characterization of a tesicicular 17,20-dihydroxy-4-pregnен-3-one (a
RT	spermiation-inducing steroid in fish) receptor from a teleost, Japanese eel (Anguilla japonica)."; FEBS Lett. 465:17(2000).
RL	-- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC	-- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
DR	EMBL; AB0032075; BRA9539.1; -.
DR	HSSP; P06536; IREG.
DR	InterPro; IPR000536; Hormone_rec_11g.
DR	InterPro; IPR001723; Steroidhormone_receptor.
DR	PFAM; PF000104; hormone_rec_1.
DR	PRINTS; PRO00105; zf-C4; 1.
DR	SMART; SM00430; Holi; 1.
DR	SMART; SM00399; Znf_C4; 1.
DR	PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
KW	DNA-binding; Nuclear protein; Receptor; Transcription regulation; Zinc-finger.
SQ	SEQUENCE 710 AA; 78819 MW; 0C8149B05CA055AA CRC64;
QY	233 TPLTCSPNANERGSRSHSPAHASNNGSPPLSSMCKSISPPSHCSVKSPVSSPNVT 292
Db	14 TPARRASPPFD---AESIKRARNLIKTESFGSYVBEIVRDDS-----NNIQ 57
QY	293 LQSSV---SSPANINNSRCSVSSPWNNTSLSSPAATVG-SICSPVNNAFSYTAG 347
Db	58 SLSSVPLMRNFGNMDTLTCAPGSGSDSEIWKDFVVPGCNVSKDTGHE-ISTKAE 115
QY	348 T\$AGS\$TLE\$VV\$P\$D\$O\$E\$K\$A\$O\$E\$V\$P\$F\$T\$E\$E\$S\$A\$T\$N\$---\$V\$T\$Q\$O\$N\$V\$Q\$Y\$K\$P\$ 402
Db	116 LSWAAAPL---SREETLAAGTVTPARPKESFTATNSSTASGSISSIKDQGSIKMEP 171
QY	403 DGA-----FSSCLGGNSKINSDDSSFSPVIKO--ESTKHS--C 436
Db	172 QSSDFCPPTANIPKLNPSYLINTASTKOLGYGEQDTSASHSSPAQIVLTDARYSADLC 231
QY	437 S-----GSTFKGNTVWPFPENDGSF\$FM\$DK\$DY\$SL\$GL\$LG\$PV\$PG\$DC\$NC----- 484
Db	232 SDNLPQPATNIKTDPC-----SSPSSFVG-----GITRASWMYSOQAIIQTLPV 276
QY	485 -EG\$GP\$PG\$IK\$Q\$P\$D\$G\$S\$Y\$P\$E\$A\$P\$S\$A\$V\$G\$V\$N\$G\$G\$S\$F\$H\$R\$G\$A\$G\$T\$S\$A\$R\$D\$Q\$ 543
Db	277 HK\$EP\$F\$R\$L\$A\$S\$A\$P\$A\$D\$S\$P\$W\$C\$O\$T\$G\$-----EDH\$Q\$D\$Y\$L\$P\$A\$G\$H\$T\$C\$K\$Y\$S\$ 326
QY	544 FQHLS\$FP\$PV\$NT\$L\$V\$E\$W\$K\$H\$G\$D\$L\$S\$R\$R\$D\$G\$Y\$P\$V\$E\$Y\$IP\$E\$N\$S\$S\$T\$L\$R\$S\$V\$T\$G\$S\$S\$R\$P\$K\$C\$ 603
Db	327 TNAYSSVLYV-----L\$P\$R\$V\$C\$ 342
QY	604 LY\$G\$D\$E\$A\$S\$G\$C\$H\$Y\$W\$T\$G\$C\$K\$Y\$F\$K\$R\$A\$V\$E\$G\$O\$H\$N\$Y\$L\$C\$A\$G\$R\$N\$D\$C\$D\$K\$R\$K\$N\$C\$P\$A\$C\$R\$L\$C\$ 663
Db	343 VLG\$D\$E\$A\$S\$G\$C\$H\$Y\$W\$T\$G\$C\$K\$Y\$F\$K\$R\$A\$V\$E\$G\$O\$H\$N\$Y\$L\$C\$A\$G\$R\$N\$D\$C\$D\$K\$R\$K\$N\$C\$P\$A\$C\$R\$L\$C\$ 402
QY	664 LQ\$G\$M\$N\$G\$A\$R\$K\$R\$K\$R\$K\$G\$K\$K\$G\$H\$E\$Q\$P\$Q\$Q\$Q\$P\$P\$P\$P\$P\$P\$Q\$S\$P\$E\$G\$T\$Y\$A\$P\$A\$E\$P\$V\$N\$T\$ 723
Db	403 YQ\$A\$G\$M\$G\$I\$L\$G\$R\$K\$K\$K\$G\$K\$A\$-----AG\$T\$Q\$A\$V\$A\$H\$S\$ 434
QY	724 VP\$Q\$L\$S\$T\$R\$S\$A\$R\$T\$P\$-----SP\$-V\$M\$V\$L\$E\$T\$E\$P\$V\$Y\$A\$G\$D\$S\$K\$P\$D\$T\$A\$E\$N\$L\$S\$T\$ 768
Db	435 T\$P\$R\$R\$L\$G\$D\$S\$O\$A\$M\$P\$L\$G\$C\$P\$G\$V\$R\$E\$H\$L\$S\$Q\$O\$S\$V\$E\$S\$T\$E\$P\$V\$Y\$G\$Y\$N\$S\$Q\$P\$M\$P\$N\$M\$L\$C\$ 494
QY	769 UNR\$A\$G\$K\$M\$Q\$V\$W\$V\$K\$A\$W\$Y\$K\$P\$F\$K\$N\$P\$L\$B\$D\$Q\$T\$T\$Y\$O\$Y\$W\$M\$C\$U\$S\$F\$A\$S\$F\$W\$R\$S\$Y\$K\$T\$N\$S\$O\$F\$Y\$ 828
Db	495 LN\$R\$C\$E\$R\$O\$L\$R\$V\$K\$W\$K\$S\$L\$P\$G\$F\$R\$S\$L\$H\$T\$N\$O\$M\$A\$Y\$O\$Y\$W\$M\$S\$M\$M\$V\$F\$S\$G\$W\$R\$S\$F\$O\$N\$V\$T\$D\$Y\$ 554
QY	829 FAD\$P\$V\$N\$E\$ 837
Db	555 FAD\$P\$LINE 563
RESULT	8
ID	09245
AC	09245; PRELIMINARY; PR#: 853 AA.
DT	01-NOV-1998 (TREMBlrel. 08, Created)
DT	01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE	ANDROGEN RECEPTOR BETA.
GN	AR BETA.
OS	Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC	Eukaryota; Metazoa; Craniata; Vertebrata; Euteleostomi;
OC	Actinopterygii; Neopterygii; Teleostei; Euteleostei; Salmonidae; Oncorhynchus.
OC	NCBI_TaxID=8022;
RN	SEQUENCE FROM N.A.
RP	MEDLINE-9910354; PubMed=10026186;
RA	Takeo J., Yamashita S.;
RT	"Two distinct isoforms of cDNA encoding rainbow trout androgen receptors.";
RL	J. Biol. Chem. 274: 5674-5680 (1999).
CC	-- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
EMBL	AB012096; BAA32785.1; -.

Query Match 17.1%; Score 756.5; DB 13; Length 710;  
 Best Local Similarity 31.4%; Pred. No. 7.1e-43;  
 Matches 210; Conservative 84; Mismatches 192; Indels 183; Gaps 20;





QY	687	EQQQQQPPPPPPQQSPEEPTVIAKAE--PSVNTALVPQ--LSITSLRATPPSPVM	740
Db	61	D----SPTKEGGQTCPGSGGLISGGKELSTSPNTNALVPHGGGLVTPYLPPSICS	115
QY	741	VLENIEPEIIVAGYDSSKRDTAENLSTLNRLACKOMQVWKWVLPFKNLPIEDQIT	800
Db	116	VLEIEPEVFAQYDNTQDFTDHLLSSINLQAGKOMRIVRKWAKVLPFGRGLPIDEQIT	175
QY	801	LIQSWMCUCLSSPALSWRSYKHTNSQFLYFAPDLVNE	837
Db	176	LIQSWMCUCLSSLSWSRSYKHTNQMLYFAPDLVNE	212
RESULT	12		
Q9GK9			
ID	Q9GK9	PRELIMINARY;	PRT; 895 AA.
AC	Q9GK9;		
DT	01-MAR-2001 (TREMBLrel. 16, Created)		
DT	01-MAR-2001 (TREMBLrel. 16, Last sequence update)		
DE	ANDROGEN RECEPTOR AR.		
OS	Sus scrofa (Pig).		
OC	Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.		
OX	NCBITaxonID=9823;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	Medline=20539123; Pubmed=11086548;		
RA	Trakooljul N., Ponsuksili S., Schellander K., Wimmers K.;		
RT	"A highly polymorphic repetitive polypyrimidine/polypurine (CCTT)n sequence in the 5' untranslated sequence of the porcine androgen receptor gene";		
RT	Anim. Genet. 31:288-289(2000).		
CC	- - - SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).		
CC	- - - SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.		
DR	EMBL; AE1617; ARG4056.1; -.		
DR	HSSP; P06536; IGDC.		
DR	InterPro; IPR010103; Androgen_recep.		
DR	InterPro; IPR005336; Hormone_rec_119.		
DR	InterPro; IPR001628; zf-C4.		
DR	Pfam; PF02166; Androgen_recep; 1.		
DR	Pfam; PF00104; hormone_rec; 1.		
DR	Pfam; PF00105; zf-C4; 1.		
DR	PRINTS; PRO0047; STRODEFINGER.		
DR	SMART; SM00430; HOLI; 1.		
DR	SMART; SM00399; Znf_C4; 1.		
DR	PROSITE; PS00031; NUCLEAR_RECECTOR; 1.		
KW	DNA-binding; Nuclear protein; Receptor; Transcription regulation; Zinc-finger.		
SEQUENCE	895 AA; 97156 MW; 923C2FDD1F7E4779 CRC64;		
RESULT	13		
P70048			
ID	P70048	PRELIMINARY;	PRT; 790 AA.
AC	P70048;		
DT	01-FEB-1997 (TREMBLrel. 02, Created)		
DT	01-JAN-1999 (TREMBLrel. 09, Last sequence update)		
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)		
DE	ANDROGEN RECEPTOR ALPHA ISOFORM.		
GN	XL ALPHA AR.		
OS	xenopus laevis (African clawed frog).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Xenopoda; Batrachia; Anura; Mesobatrachia; Pipidae; Xenopidae; Xenopidae: Xenopus.		
OC	NCBI_TaxID=8355;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	Medline=9337678; Pubmed=7690145;		
RA	Fischer L., Catz D., Kelley D.;		
RT	"An androgen receptor mRNA isoform associated with hormone-induced cell proliferation";		
RT	Proc. Natl. Acad. Sci. U.S.A. 90:8254-8258(1993).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RX	Medline=95324753; Pubmed=7601302;		
RA	Fischer L.M., Catz D., Kelley D.B.;		
RT	"Androgen-directed development of the Xenopus laevis larynx: control of androgen receptor expression and tissue differentiation";		
RT	Dev. Biol. 170:115-126(1995).		
RN	[3]		
RP	SEQUENCE FROM N.A.		
RA	Kelley D.B., Kamenetz F.R., Kelley D.B., Badea T.C.;		
RL	Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.		
CC	- - - SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).		
CC	- - - SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.		
DR	EMBL; U67129; AAC97386.1; -.		
DR	HSSP; P06536; IGDC.		

DR InterPro; IPR001103; Androgen\_recep.  
 DR InterPro; IPR000536; Hormone\_rec\_lig.  
 DR InterPro; IPR001628; zf-C4.  
 DR Pfam; PF02166; Androgen\_Recep; 3.  
 DR Pfam; PF00104; hormone\_rec; 1.  
 DR Pfam; PF00105; zf-C4; 1.  
 DR PRINTS; PRO0047; STROIDFINGER.  
 DR SMART; SM00430; HOLT; 1.  
 DR PROSITE; PS00031; NUCLEAR\_RECECTOR; 1.  
 KW DNA-binding; Nuclear protein; Receptor; Transcription regulation;  
 SEQUENCE 790 AA; 86973 MW; 9EFC136CCCC3906 CRC64;

Query Match 16.7%; Score 739; DB 13; Length 790;  
 Best Local Similarity 31.1%; Pred. No. 1. 3e-41; Index 204; Gaps 27;  
 Matches 215; Conservative 79; Mismatches 204; Indels 194; Gaps 27;

Qy 241 AENRGSRSHSPAHASNVGSPPLSSPLSMKSSISPPSHCSVSKPVSPNNTLRSVV- 299  
 Db 51 SEAPGTHRWSSEASPOD-GTPLN-----PWTIHPAPWRAEQEARAPONPAGRTEGAOF 102

Qy 300 ----PANT----NNSRSVSVSPTNNTNRSTLSP--AASTVGUSICPVN----- 338  
 Db 103 PALGDCPTEKELIGBQSGRILSEETPAKEEGSPPPEGISDAKELCKAVSVSIGLSM 162

Qy 339 NAFSYIASGTSAGSSTLRD--WVSPDT-----QEKGAEVFPKPKEEVESAISNG 387  
 Db 163 EALEHLSAG--AGEAQORGDMYAHPTDKQVAEEDKSUTRDEPFRRSQ-----SNF 215

Qy 388 VTGQLNIVQYIKPEP--DGAFSSCIGGNSKINSDSSFSVPIKOBSTKHSC----SGT 439  
 Db 216 ATGK-----SPEDGGGGGSSAGGSEEKEQPCIDALPEPAGGYRHARAMELTPLT 268

Qy 440 SFKGNPTVNPPEPMGS--SFSEMDKDVSLSGLGP----- 475  
 Db 269 LYK-----PTAFMEESPYPSS---RDFYSFQMALAPHGRIKVNPMEYGGANGAAGR 318

Qy 476 --PVCF-----DGCECGSGPVGKIOP-----DDGSIYPEASIPSSA 512  
 Db 319 YSELSGFAHAGATAGWHTLEEEQGSSFEAEGPSYSPRSHGPGADGEPSDAMYRAPT 378

Qy 513 IVGVNNSGGQSFHYRGAQGTISRSARDOSFOHLSFPVNTLYESWKS--HGDLSRR 570  
 Db 379 MIG-----RVPYSG----- 408

Qy 571 SDG-----VPYLETPENVSSTLRSVSTGSSRSPKICLWGDDESGCHGIVWTCGCK 625  
 Db 409 LEGGRDHLLPIDYFP-----PORTCLICGDEASGHCHYGAITCGCKV 451

Qy 626 FFKRAVEGQHNYLCAGRNDCTIDKIRKKNPACRQKCLQGMGNARGKKGKKGH 685  
 Db 452 FFKRAEGKOKYKYLASCNRDCTIDKRRKNCPSCLRKCYAGMTGARKKKKGKQAE 511

Qy 686 EEQQQQQQQPPPPPPPPQSPERGTIAKPEVKSPVNTLVALPOLSTISRALTPSPAVLENT 745  
 Db 512 ELDGSSVQ-----GEGSKELSPGM-----IPOLEGTS-COPIFANLAEI 551

Qy 746 EPEIVVAGYDSSKSPDTAENLISTLRLAKOMIQWKAWLPGKNLPLEDQILOYS 805  
 Db 552 EPVWVCAHGHDNQPDPSFALLSSNLBGEROLVHVYKWAALPGFERNLHYSDQMVQYS 611

Qy 806 WMCLSSFALSRSYKHTNSQSLFIRDLYNE 837  
 Db 612 WNGLMFAMFWRSFRKVNNSRMLYFADLVNE 643

SEQUENCE FROM N.A.

RJ Jin C.H., Urcan-Bisel M.S.; Schrader W.T.;  
 RT "Androgen receptor sequences in human mammary carcinoma MDA-MB-453  
 RT cells";  
 RL Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.  
 CC -I- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).  
 CC -I- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.  
 DR EMBL; AF162704; AAD5921.1; -.  
 DR HSSP; P0535; ICD;  
 DR InterPro; IPR01103; Androgen\_recep.  
 DR InterPro; IPR000536; Hormone\_rec\_lig.  
 DR InterPro; IPR001628; zf-C4.  
 DR Pfam; PF02166; Androgen\_recep; 1.  
 DR Pfam; PF00104; hormone\_rec; 1.  
 DR Pfam; PF0105; zf-C4; 1.  
 DR PRINTS; PRO0047; STROIDFINGER.  
 DR SMART; SM00430; HOLT; 1.  
 DR PROSITE; PS00031; NUCLEAR\_RECECTOR; 1.  
 KW DNA-binding; Nuclear protein; Receptor; Transcription regulation;  
 SEQUENCE 906 AA; 97884 MW; 0A1FA8802B2EDDAF CRC64;

Query Match 16.5%; Score 729.5; DB 4; Length 906;  
 Best Local Similarity 30.1%; Pred. No. 6. 6e-11; Index 229; Gaps 30;  
 Matches 229; Conservative 76; Mismatches 205; Indels 251; Gaps 30;

Qy 238 SPNAENRGSRSHSPAHASNVGSPPLSSPLSMKSSISPPSHCSVSKPVSPNNTLRSVV 297  
 Db 89 SFQAHRRGPTGIL-----WLDEEQOP-SQPSALECHPERGCVCPEP-----GAVAASK 136

Qy 298 SSPANINNSRSVSSPNTNNTNRSTLSPASIVGUSICSPNNAFYTASOTSGSSTLRD 357  
 Db 137 GLPQQL-----PAPPDED-----SAASNL-SLGP-----TEPGLSSCSADLK 176

Qy 358 VVPSDPOEKGAEVFPKPKEEVESAISNGVTGQLNIVQYIKPEPDGAFFSS--CLGGN 414  
 Db 177 ILSEASTMQLQQ-----QEAVSESSSSRA-----RESGAFSSKDNWLGT 222

Qy 415 SKINS-----SFSVPTIQUESTKHSCTGTSFKGN-----PTVNPFP----- 451  
 Db 223 STISDNAKELKAVSVMSMGIVLVEALBLHSPGEQLRDCMAYPLGVPPAVRPTPCAPLAE 282

Qy 452 -----FMDGSWSFMDKDYVLSLSGLGPVPGDF----NOEGS----- 487  
 Db 283 CKGSLIUDSAGKSKTDETAEV--SPERGGYTGKLGEBESLGLGSSAAGSSGTTLEPLSTL 340

Qy 488 -----GFPVGIQEP----- 501

Db 341 YKSGALDEAMAYQSRYYNNFLALGPPPPPPPHARAKLENLDYSSAAAACCR 400

Qy 502 YYPEAPSIPSAVGVNNG-----GOSFY----- 526

Db 401 YGDLASLHGAAAGPGSGSSAASSSWHILFTAEGOLYLGPGCGGGGGGGGGGG 460

Qy 527 IGAQTSILSRSARDOSFOH----- 562

Db 461 AGAVAPYGYTRPQGLAQSDFTADVWYPPGMWSRVPSPTCVKSENGPWNDSYSGP 520

Qy 563 HGD-LSSRSRDGYPVLEYIPENVSSTLRSVSTGSSRSPKICLVCGLDESGCHGVTC 620

Db 401 YGDLASLHGAAAGPGSGSSAASSSWHILFTAEGOLYLGPGCGGGGGGGGGGG 460

Qy 521 YGDRMTRARHVLPDYFP----- 563

RESULT 14  
 Q9UN21 PRELIMINARY; PRT; 906 AA.  
 ID Q9UN21  
 AC Q9UN21; 01-MAY-2000 (TREMBrel. 13, Created)

QY 621 GSCKVFFKRAVEQHNYLCAGRNDCLIDKIRRNCPACRLQKCLQAGMNLGARKSKKLKG 680  
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
 Db 564 GSCKVFFKRAEGKOKYLICASRNDCTDKFRKNCPSCLRKCYEAGMTLGRKKLGN 623  
 QY 681 LKGTHESQPOQDOPPPPPPPSPSPEEGTYIAPAKEPSYNTALVPOLSTISR--ALTP 736  
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
 Db 624 LK-LQEGEASS---TSPTEET---OKLTVSHIEGYECOP 658  
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
 QY 737 SPVMLEIEPEWVAGYDSSRPTAENLSTNLLAGKOMIQVKWAKVLPGFKNPLP 796  
 ;||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
 Db 659 IFLNWLAEIPEGVCAHGDNQDSDFAALSSNELGERLVHVKWAKALPGLRNLD 718  
 ;||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
 QY 797 DQITLIQSWMCISFALSWSRSYKHTNSQFLYFADLVNE 837  
 ;||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
 Db 719 DQMVQIYQSWMGIMVFAMGWRSTINVNSRMLYFADLVNE 759  
 ;||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
 RESULT 15  
 Q9IGV9 PRELIMINARY; PRT; 848 AA.  
 ID Q9IGV9  
 AC 01-MAY-1999 (Tremblrel. 10, Created)  
 DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)  
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)  
 DE ANDROGEN RECEPTOR ALPHA.  
 OS Anguilla Japonica (Japanese eel).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;  
 Actinopterygii; Neopterygii; Teleostei; Anguilliformes; Anguilloidei;  
 OC Anguillidae; Anguilla.  
 NCBI-TaxID=797;  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RC RP  
 TISSUE=TESTIS;  
 RX MEDLINE:99119319; PubMed=9918846;  
 RA Todo T., Icheku T., Kobayashi T., Nagahama Y.;  
 RT Fish androgen receptor: cDNA cloning, steroid activation of  
 transcription in transfected mammalian cells, and tissue mRNA  
 levels.",  
 RL Biophys. Res. Commun. 254:378-383(1999).  
 CC -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).  
 CC -!- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.  
 DR EMBL: AB23960; BAA75464.1; -.  
 DR HSSP: P0536; LGDC.  
 DR InterPro: IPR0103; Androgen\_recep.  
 DR InterPro: IPR00536; Hormone\_rec\_lig.  
 DR InterPro: IPR001628; zf-C4.  
 DR Pfam: PF02166; Androgen\_rec.  
 DR Pfam: PF00104; Hormone\_rec; 1.  
 DR Pfam; PF00105; zf-C4; 1.  
 DR PRINTS; PR00047; STEROIDFINGER.  
 DR SMART; SM00430; HOLI; 1.  
 DR PROSITE; PS00399; Znf\_C4; 1.  
 DR DNA-binding; NUCLEAR\_RECEPTOR; 1.  
 KW Zinc-finger; Nuclear protein; Receptor; Transcription regulation;  
 KW SEQUENCE 848 AA; 94692 MW; A8889AF/F2E50D3E CRC64;

Query Match 16.4%; Score 727; DB 13; Length 848;  
 Best Local Similarity 31.9%; Pred. No. 8.9e41; Mismatches 27;  
 Matches 217; Conservative 87; Mismatches 244; Indels 132; Gaps 27;

QY 214 SSTMASFGSPVPHSITQGPPLTSPNAENRGSSHSP---ANASNVGSPLOSSMK 269  
 | :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|  
 Db 99 SDAEARPGIFS-ESSLDTGBCITCKLQSDNGVRASGPLPGSSGCNSQSSACTSQO 157  
 QY 270 SSISSPSPHSQVKSPVSPSPNVTLRRSSPSSPANTINNSRCVSSPSN-TNNRSTTSSPA 327  
 | :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|  
 Db 158 RETTSQSDTCAGES-CSEHQAT---TISETARELCAVSVLSIGLNLDNDMDLDSNQI 212  
 QY 328 STVGSGCSPNNAFASVTSAGSSTL-RDVV----PSPDQKEKA----QEV 372  
 | :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|  
 Db 213 SSTESTSDTSQAYLFESSPGYTGIVGLNALVRDCKCOSAREGTSTQDYDRGAMFKINRVNDL 272

QY 373 PPKPTEEVESATN-----GVTGOLINTIVOKYK PEPDGAFGSSCLGGNSKINSDDSS 424  
 | :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|  
 Db 273 PLQAPAPRHTSISDAKWDMEAGLCAPMHEKSEKGANMDGAHSTS-----VFSQFDQL 325  
 QY 425 VLIKQESTKHKCSGTSFKGNPPTVNPPFPMDGSYSFEMDDKDYYSLSGLLGPVPGFDGNC 484  
 :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|  
 Db 326 LPV--NASHSQNVSVREVEQSFDFSPIL-----YKS-----PCIQNA 361  
 QY 485 EGSGFPVGTKQEPDGS-----YYPEASIPSSA--IVGVNSGG--QSFPH-- 524  
 | :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|  
 Db 362 EKYNQVQDATIKSEDGKUTSEREWG-QYRYESCSPSAPPRHCAHQNRACGPYNOFFNP 421  
 QY 525 YRGAQGTISLSRSARDQFQHLSFPPVVNE--SWKSHGDLSRSRPGYPVLEY-- 579  
 ;| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|  
 Db 422 FEVAKGVV--SREGSYLIEH--GFP--NINLARTPYSGSLKNELGDRLSGPYPDVSYR 473  
 QY 580 -IPENYSSSTLRSVSTGSSRSKICLVCVGDEASGCHIVGTVGCGSKVFRKRAVEQHNY 637  
 ||| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|  
 Db 474 EGERENVFPEF----FFPPORTCLICGDEASGHYGAATCGSKVFRKRAEGKOKY 527  
 QY 638 LCAGRNCIIDIKIRRNCPACRLQKCLQAGMNLGARKSKKKLGLKGTHEEQPOQQOPPP 697  
 ||| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|  
 Db 528 LCASINDCTIDKIRRNCPACRKRCRPAAGMVLGARLKKGOMRA-----PE 575  
 QY 698 PPPQSPEEGTYIAPAKEPSYNTALVPOLSTISRALTPSPVNLNIEPIHVAGYDSS 757  
 ;| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|  
 Db 576 DGOGQPAEAELSVSPKVDLGFHTQ-----SMFLN----ILEAIEPVNVAGHDYQ 622  
 QY 758 KPDTAENLSTLNRLAGKOMIQVKWAKVLPGFKNPLDEDQITLIOSWMLSSELSWR 817  
 ;| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|  
 Db 623 QPSSAASLTSNLNLGERQVLUKVAKGMPGRSLVYDQMTVIOSHWMVNFALGWR 682  
 QY 818 SYKHTNSOPLYFADLVNE 837  
 ;| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|  
 Db 683 SFKVKNSRMLYFADLVNE 702

Search completed: September 13, 2002, 10:21:28  
 Job time: 302 sec

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